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protein database search, using Smith-Waterman algorithm

not generated.

1 GINLHWLQDQEPDGTIKR 17

PAM 150

165420 seqs, 49795644 residues

## Listing first 45 summaries

sptrembl6

13:sp\_vertebrate 14:sp\_virus

Mean 27.617; Variance 43.342; scale 0.637

and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	73	55.7	456	2	047315	TRANSPOSASE IS91.	6.71e-07
2	69	52.7	365	14	086302	SIGMA 3.	3.47e-01
3	69	52.7	365	14	086293	SIGMA 3.	3.47e-01
4	69	52.7	365	14	086301	SIGMA 3.	3.47e-01
5	69	52.7	365	14	086297	SIGMA 3.	3.47e-01
6	69	52.7	365	14	086294	SIGMA 3.	3.47e-01
7	69	52.7	365	14	086299	SIGMA 3.	3.47e-01
8	69	52.7	365	14	086296	SIGMA 3.	3.47e-01
9	68	51.9	465	10	064733	PURATIVE INDOLE-3-ACET	5.19e-01
10	66	50.4	328	10	023300	CARNITINE RACEMASE HOM	1.15e+00
11	66	50.4	426	14	082315	HEMAGGLUTININ PRECURSO	1.15e+00
12	66	50.4	365	14	096842	OUTER-CAPSID PROTEIN S	1.15e+00
13	66	50.4	365	14	096840	OUTER-CAPSID PROTEIN S	1.15e+00
14	66	50.4	365	14	096839	OUTER-CAPSID PROTEIN S	1.15e+00
15	66	50.4	365	14	096841	OUTER-CAPSID PROTEIN S	1.15e+00
16	66	50.4	365	14	086300	SIGMA 3.	1.15e+00
17	66	50.4	365	14	086295	SIGMA 3.	1.15e+00
18	66	50.4	365	14	096838	OUTER-CAPSID PROTEIN S	1.15e+00
19	66	50.4	365	14	086303	SIGMA 3.	1.15e+00
20	66	50.4	365	14	096827	OUTER-CAPSID PROTEIN S	1.15e+00

21	66	365	14	086292	SIGMA 3.	1.15e+00
22	66	50.4	365	14	SIGMA 3.	1.15e+00
23	65	49.6	136	4	DI29K1.1.	1.70e+00
24	65	49.6	563	14	INFLUENZA T51.1/A/EPV/	1.70e+00
25	65	49.6	563	14	INFLUENZA A/EPV/ROSTOC	1.70e+00
26	63	48.1	361	14	HEMAGGLUTININ PRECURSO	3.70e+00
27	63	48.1	362	14	HEMAGGLUTININ PRECURSO	3.70e+00
28	63	48.1	362	14	HEMAGGLUTININ PRECURSO	3.70e+00
29	63	48.1	365	14	SIGMA 3.	3.70e+00
30	63	48.1	373	14	HEMAGGLUTININ PRECURSO	3.70e+00
31	63	48.1	560	14	HEMAGGLUTININ PRECURSO	3.70e+00
32	63	48.1	560	14	HEMAGGLUTININ PRECURSO	3.70e+00
33	63	48.1	562	14	HEMAGGLUTININ PRECURSO	3.70e+00
34	63	48.1	562	14	HEMAGGLUTININ PRECURSO	3.70e+00
35	63	48.1	562	14	HEMAGGLUTININ PRECURSO	3.70e+00
36	63	48.1	563	14	HEMAGGLUTININ PRECURSO	3.70e+00
37	63	48.1	564	14	HEMAGGLUTININ PRECURSO	3.70e+00
38	63	48.1	697	5	RNA QUANTILYTRANSEFERAS	5.42e+00
39	62	47.3	322	2	REGION B OF COSMID SCT	5.42e+00
40	62	47.3	362	14	HEMAGGLUTININ PRECURSO	5.42e+00
41	62	47.3	543	14	MULTIGENE FAMILY 530 P	5.42e+00
42	62	47.3	763	3	DNATOPISOISOMERASE I	5.42e+00
43	62	47.3	985	13	RECEPTOR TYROSINE KINA	5.42e+00
44	61	46.6	370	14	HEMAGGLUTININ PRECURSO	7.91e+00
45	61	46.6	545	14	VIRAL FUSION PROTEIN (	7.91e+00

## ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	426 AA.
ID	047315			
AC	047315;			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)			
DE	TRANSPOSASE IS91.			
GN	TNPA.			
OS	ESCHERICHIA COLI.			
OG	PLASMID PSU2911.			
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;			
OC	ENTEROBACTERIACEAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 92138630.			
RA	MENDIOLA M.V., JUBETE Y., LA CRUZ F.;			
RL	BACTERIOL. 174:1345-1351(1992).			
LN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 92335017.			
RA	MENDIOLA M.V., DE LA CRUZ F.;			
RL	NUCLEIC ACIDS RES. 20:3521-3521(1992).			
DR	EMBL; X17114; G41842; -.			
KW	PLASMID.			
SO	SEQUENCE	426 AA;	49982 MW;	226BB3E5 CRC32;
Query Match				
Best Local Similarity		55.78;	Score 73;	DB 2; Length 426;
Matches		5; Conservative	7; Mismatches	1; Indels 0; Gaps 0;
DB	16 LNWLEKQEGSVR	28		
QY	53 LHWLQEPDGTIK	65		
RESULT				
ID	086302	PRELIMINARY;	PRT;	365 AA.
AC	086302;			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)			
DE	SIGMA 3.			
GN	S4.			
OS	REOVIRUS.			

OC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SEROTYPE 3;  
RX MEDLINE: 95074914.  
RA KEDL R., SCHMECHTEL S.C., SCHIFF L.A.;  
RL J. VIROL. 69:552-559(1995).  
DR EMBL: U15083; G706880; -  
SQ SEQUENCE 365 AA; 41054 MM; 594C3CEF CRC32;  
SO  
Query Match 52.7%; Score 69; DB 14; Length 365;  
Best Local Similarity 40.0%; Pred. No. 3.47e-01;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
DB 129 VELMWLOVDPDSMR 143  
QY 51 INLHMLQOEPDGTIK 65  
RESULT 3 PRELIMINARY; PRT: 365 AA.  
AC 086293;  
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)  
DE SIGMA 3.  
GN S4.  
OS REOVIRUS.  
OC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SEROTYPE 3;  
RX MEDLINE: 95074914.  
RA KEDL R., SCHMECHTEL S.C., SCHIFF L.A.;  
RL J. VIROL. 69:552-559(1995).  
DR EMBL: U15074; G706862; -  
SQ SEQUENCE 365 AA; 41032 MM; D074A4E4 CRC32;  
SO  
Query Match 52.7%; Score 69; DB 14; Length 365;  
Best Local Similarity 40.0%; Pred. No. 3.47e-01;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
DB 129 VELMWLOVDPDSMR 143  
QY 51 INLHMLQOEPDGTIK 65  
RESULT 4 PRELIMINARY; PRT: 365 AA.  
AC 086301;  
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)  
DE SIGMA 3.  
GN S4.  
OS REOVIRUS.  
OC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SEROTYPE 3;  
RX MEDLINE: 95074914.  
RA KEDL R., SCHMECHTEL S.C., SCHIFF L.A.;  
RL J. VIROL. 69:552-559(1995).  
DR EMBL: U15082; G706878; -  
SQ SEQUENCE 365 AA; 41123 MM; 1A54DC7D CRC32;  
SO  
Query Match 52.7%; Score 69; DB 14; Length 365;  
Best Local Similarity 40.0%; Pred. No. 3.47e-01;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
DB 129 VELMWLOVDPDSMR 143  
QY 51 INLHMLQOEPDGTIK 65

RESULT 5  
ID 086297 PRELIMINARY; PRT: 365 AA.  
AC 086297;  
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)  
DE SIGMA 3.  
GN S4.  
OS REOVIRUS.  
OC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SEROTYPE 3;  
RX MEDLINE: 95074914.  
RA KEDL R., SCHMECHTEL S.C., SCHIFF L.A.;  
RL J. VIROL. 69:552-559(1995).  
DR EMBL: U15078; G706870; -  
SQ SEQUENCE 365 AA; 41018 MM; 139ED362 CRC32;  
SO  
Query Match 52.7%; Score 69; DB 14; Length 365;  
Best Local Similarity 40.0%; Pred. No. 3.47e-01;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
DB 129 VELMWLOVDPDSMR 143  
QY 51 INLHMLQOEPDGTIK 65  
RESULT 6 PRELIMINARY; PRT: 365 AA.  
ID 086294;  
AC 086294;  
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)  
DE SIGMA 3.  
GN S4.  
OS REOVIRUS.  
OC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SEROTYPE 1;  
RX MEDLINE: 95074914.  
RA KEDL R., SCHMECHTEL S.C., SCHIFF L.A.;  
RL J. VIROL. 69:552-559(1995).  
DR EMBL: U15075; G706864; -  
SQ SEQUENCE 365 AA; 40993 MM; 251F3243 CRC32;  
SO  
Query Match 52.7%; Score 69; DB 14; Length 365;  
Best Local Similarity 40.0%; Pred. No. 3.47e-01;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
DB 129 VELMWLOVDPDSMR 143  
QY 51 INLHMLQOEPDGTIK 65  
RESULT 7 PRELIMINARY; PRT: 365 AA.  
ID 086299;  
AC 086299;  
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)  
DE SIGMA 3.  
GN S4.  
OS REOVIRUS.  
OC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SEROTYPE 3;  
RX MEDLINE: 95074914.  
RA KEDL R., SCHMECHTEL S.C., SCHIFF L.A.;



RL J. VIROL. 69:552-559(1995).  
 DR EMBL; U15080; G706874; -  
 SQ SEQUENCE 365 AA; 41074 MW; 0B2EE93D CRC32;

Query Match 52.7%; Score 69; DB 14; Length 365;  
 Best Local Similarity 40.0%; Pred. No. 3.47e-01;  
 Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 129 VELNMLQVDPDSMFR 143  
 ::|||::|||::  
 QY 51 INLHMLQOEPDGTIK 65

RESULT 8 PRELIMINARY; PRT; 365 AA.  
 AC 086296.  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)  
 DT SIGMA 3.

OS REOVIRUS.  
 OC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SEROTYPE 3;  
 RX MEDLINE; 95074914.  
 RA KEDL R., SCHECHTEL S.C., SCHIFF L.A.;  
 RL J. VIROL. 69:552-559(1995).  
 DR EMBL; U15077; G706868; -  
 SQ SEQUENCE 365 AA; 41090 MW; 58C38B31 CRC32;

Query Match 52.7%; Score 69; DB 14; Length 365;  
 Best Local Similarity 40.0%; Pred. No. 3.47e-01;  
 Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 129 VELNMLQVDPDSMFR 143  
 ::|||::|||::  
 QY 51 INLHMLQOEPDGTIK 65

RESULT 9 PRELIMINARY; PRT; 455 AA.  
 AC 064733.  
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DT PUTATIVE INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE.  
 DT T27E13.12.

OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;  
 OC CAPRIFALES; CRUCIFERAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA ROUNSELEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,  
 RA STYKE S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,  
 RA SOMERVILLE C.R., VENTER J.C.;  
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; AC004165; G3150406; -  
 KW TRANSFERASE.

Query Match 51.9%; Score 68; DB 10; Length 455;  
 Best Local Similarity 33.3%; Pred. No. 5.19e-01;  
 Matches 4; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Db 260 IOWLEBOEGSV 271  
 ::|||::|||::  
 QY 53 LHMLOQEPDGTI 64

RESULT 10

ID 023300 PRELIMINARY; PRT; 238 AA.

AC 023300;  
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DE CARANTINE RACEMASE HOMOLOG.  
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;  
 OC CAPRIFALES; CRUCIFERAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA BEVAN M., STEKEMA W., MURPHY G., WAMBUIT R., POHL T., TERRY N.,  
 RA KREIS M., KAVANAGH T., ENTIAN K.D., RIEGER M., JAMES R.,  
 RA PUTIGOMENECHE P., HATZIOPOULOS P., OBERMAIER B., DIESTERHOFF A.,  
 RA JONES J., PALME K., ANSORGE W., DEISENT M., BANCROFT I., MENES H.W.,  
 RA SCHUELLER C., CHALWATZIS N.;  
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;  
 RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; Z97336; E327452; -  
 DR PFAM; PF00378; ECH.  
 SQ SEQUENCE 238 AA; 25595 MW; AF74F9CD CRC32;

Query Match 50.4%; Score 66; DB 10; Length 238;  
 Best Local Similarity 47.1%; Pred. No. 1.15e+00;  
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 60 GFDLMAQSGAIAIKR 76  
 ::|||::|||::  
 QY 50 GINLHMLQOEPDGTIKR 66

RESULT 11 PRELIMINARY; PRT; 356 AA.

AC 082515;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE HEMAGGLUTININ PRECURSOR (FRAGMENTS).  
 GN HA.  
 OS INFLUENZA A VIRUS.  
 OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A/TURKEY/MINNESOTA/1237/80 (H7N3);  
 RX MEDLINE; 95297170.  
 RA ROHM C., HORIMOTO T., KAWAKA Y., SUSS J., WEBSTER R.G.;  
 RL VIROLOGY 209:664-670(1995).  
 DR EMBL; U20466; G902767; -  
 DR PFAM; PF00509; Hemagglutinin.

FT SIGNAL. 1 18 POTENTIAL.  
 FT CHAIN 19 >339 HEMAGGLUTININ 1 CHAIN.  
 FT NOK\_CONS 339 340  
 FT CHAIN 340 >356 HEMAGGLUTININ 2 CHAIN.  
 FT NOK\_TER 356 356  
 SQ SEQUENCE 356 AA; 38596 MW; 4C593717 CRC32;

Query Match 50.4%; Score 66; DB 14; Length 356;  
 Best Local Similarity 42.9%; Pred. No. 1.15e+00;  
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 239 IDFMILLDPNDTV 252  
 ::|||::|||::  
 QY 51 INLHMLQOEPDGTI 64

RESULT 12 PRELIMINARY; PRT; 365 AA.  
 ID 098642;  
 AC 098642;  
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)

DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
DE OUTER-CAPSID PROTEIN SIGMA 3.  
GN S4.  
OS REOVIRUS.  
OC VIRIDAE: DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-L/T2+C:  
RA WETZEL J.D., WILSON G.J., BAER G.S., DUNNIGAN L.R., WRIGHT J.P.,  
TANG D.S., DERMODY T.S.;  
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U63309; G1518832; -  
SO SEQUENCE 365 AA; 40989 MW; 5B158A9C CRC32;

Query Match 50.4%; Score 66; DB 14; Length 365;  
Best Local Similarity 33.3%; Pred. No. 1.15e+00;  
Matches 5; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

129 VELNMLQVDPNSMR 143  
QY ::|||::|::|::  
51 INLHMLQOEPDGTIK 65

RESULT 13  
ID 098640 PRELIMINARY; PRT; 365 AA.  
AC 098640:  
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)  
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
DE OUTER-CAPSID PROTEIN SIGMA 3.  
GN S4.  
OS REOVIRUS.  
OC VIRIDAE: DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-L/C:  
RA WETZEL J.D., WILSON G.J., BAER G.S., DUNNIGAN L.R., WRIGHT J.P.,  
TANG D.S., DERMODY T.S.;  
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U63307; G1518828; -  
SO SEQUENCE 365 AA; 41032 MW; 3F472E32 CRC32;

Query Match 50.4%; Score 66; DB 14; Length 365;  
Best Local Similarity 33.3%; Pred. No. 1.15e+00;  
Matches 5; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

129 VELNMLQVDPNSMR 143  
QY ::|||::|::|::  
51 INLHMLQOEPDGTIK 65

RESULT 14  
ID 098639 PRELIMINARY; PRT; 365 AA.  
AC 098639:  
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)  
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
DE OUTER-CAPSID PROTEIN SIGMA 3.  
GN S4.  
OS REOVIRUS.  
OC VIRIDAE: DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PI1A1:  
RA WETZEL J.D., WILSON G.J., BAER G.S., DUNNIGAN L.R., WRIGHT J.P.,  
TANG D.S., DERMODY T.S.;  
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U63306; G1518826; -  
SO SEQUENCE 365 AA; 41061 MW; 1AE1ACD8 CRC32;

Query Match 50.4%; Score 66; DB 14; Length 365;  
Best Local Similarity 33.3%; Pred. No. 1.15e+00;

Matches 5; Conservative 8; Mismatches 2; Indels 0; Gaps 0;  
Db 129 VELNMLQVDPNSMR 143  
QY ::|||::|::|::  
51 INLHMLQOEPDGTIK 65

RESULT 15  
ID 098641 PRELIMINARY; PRT; 365 AA.  
AC 098641:  
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)  
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
DE OUTER-CAPSID PROTEIN SIGMA 3.  
GN S4.  
OS REOVIRUS.  
OC VIRIDAE: DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-L/T2+T3:  
RA WETZEL J.D., WILSON G.J., BAER G.S., DUNNIGAN L.R., WRIGHT J.P.,  
TANG D.S., DERMODY T.S.;  
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U63308; G1518830; -  
SO SEQUENCE 365 AA; 41080 MW; D4C19A6F CRC32;

Query Match 50.4%; Score 66; DB 14; Length 365;  
Best Local Similarity 33.3%; Pred. No. 1.15e+00;  
Matches 5; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Db 129 VELNMLQVDPNSMR 143  
QY ::|||::|::|::  
51 INLHMLQOEPDGTIK 65

Search completed: Tue Apr 20 13:58:25 1999  
Job time : 29 secs.



DR WPI: 97-341690/31.  
 DR N-PSDB: T85149.  
 PT Monoclonal anti-idiotypic antibody 11D10 - elicits immune response  
 PT against human milk fat globule disease associated tumours,  
 PS especially breast cancer  
 PS Claim 9: Page 94: 130pp: English.  
 CC This polypeptide sequence comprises the light chain variable region  
 CC (VL) of monoclonal anti-idiotypic antibody 11D10 produced by  
 CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising  
 CC naive mice with MC-10 anti-HMG antibody to obtain an anti-idiotypic  
 CC response. It elicits an immune response against a specific epitope  
 CC of a high mol. wt. mucin of human milk fat globule (HMF). It  
 CC induces an immunological response to HMF in mice, rabbits, monkeys  
 CC and patients with advanced HMF-associated tumours. Pharmaceutical  
 CC compositions and vaccines comprising 11D10, 11D10 polypeptides  
 CC and/or 11D10 polynucleotides (see also T85149-50) are claimed.  
 CC Also claimed are diagnostic kits and methods of using 11D10, 11D10  
 CC polypeptides and/or 11D10 polynucleotides, including methods of  
 CC treating HMF-associated tumours. 11D10 is also used in a claimed  
 CC method of palliating HMF-associated disease and in claimed kits to  
 CC detect or quantify anti-HMF antibody.  
 SQ Sequence 145 AA;

Query Match 100.0%; Score 68; DB 25; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 1.06e+01;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 esedfvay 107  
 |||||  
 99 ESEDFVAY 107

RESULT 2  
 ID R80078 standard; Protein; 90 AA.  
 AC R80078;  
 DE 22-MAY-1996 (first entry)  
 DE Mouse derived light chain RT3 phage antibody pattern A.  
 KM Light chain; RT3; murine; catalytic antibody; bacteriophage;  
 KM pattern A.  
 OS Mus musculus.  
 PH Key  
 FT region Location/Qualifiers  
 FT 1..15  
 FT /note= "framework region 1"  
 FT 16..26  
 FT /note= "complementarity determining region 1"  
 FT 27..40  
 FT /note= "framework region 2"  
 FT 41..47  
 FT /note= "complementarity determining region 2"  
 FT 48..78  
 FT /note= "framework region 3"  
 FT 79..88  
 FT /note= "complementarity determining region 3"  
 FT 89..90  
 FT /note= "framework region 4  
 FT N-terminal fragment"

W09527045-A1.  
 PD 12-OCT-1995.  
 PD 30-MAR-1994; U03420.  
 PR 30-MAR-1994; WO-U03420.  
 PA (IGEN-) IGEN INC.  
 PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;  
 PI Martin MT, McCafferty J, Smith RG, Tlmas RC, Williams RO;  
 PI WPI: 95-358624/46.  
 DR N-PSDB: T04625.  
 PT Production of catalytic antibodies displayed on phage - by  
 PT generating a gene library of antibody-derived domains and expressing  
 PT it in phage vectors  
 PS Disclosure: Fig 9; 133pp: English.  
 CC T04625 encodes R80078 mouse derived light chain RT3 phage antibody.  
 CC The DNA was used in the prepn. of catalytic antibody (CA) producing  
 CC bacteriophage. The CAs can be used to activate/deactivate a  
 CC biological function in an animal by enhancing the rate of cleavage,

CC or formation of a specific bond within a mol. in vivo.  
 SQ Sequence 90 AA;

Query Match 94.1%; Score 64; DB 16; Length 90;  
 Best Local Similarity 88.9%; Pred. No. 2.34e+01;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 69 esedfvay 77  
 |||||  
 99 ESEDFVAY 107

RESULT 3  
 ID R78972 standard; Protein; 107 AA.  
 AC R78972;  
 DE 21-DEC-1995 (first entry)  
 DE Light chain variable region for monoclonal antibody 5B6.  
 KM Monoclonal antibody; heavy metal; mercury; variable region;  
 KM light chain.  
 OS Synthetic.  
 PN W09520607-A.  
 PD 03-AUG-1995.  
 PF 27-JAN-1995; U01199.  
 PR 27-JAN-1994; US-187407.  
 PA (BRON-) BRONERASKA INC.  
 PI Lopez O, Wagner FW, Wylie DE;  
 PI WPI: 95-275415/36.  
 DR N-PSDB: 097510.  
 PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from  
 PT monoclonal antibodies, used for detecting, removing, adding or  
 PT neutralising heavy metals  
 PS Claim 23: Page 70; 106pp: English.  
 CC Hybridoma antibodies have been produced with the spleen cells of  
 CC BALB/c mouse that had received multiple injections of mercuric ions  
 CC reacted with glutathione to produce a mercuric ion coordinate  
 CC hemocyanin (KLN). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,  
 CC 5B6 and 3E8) were producing MAb that were strongly positive  
 CC against glutathione-mercuric ions but negative against glutathione  
 CC without mercuric ions. RNA was isolated from hybridoma cells with  
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed  
 CC by MLV reverse transcriptase. The primers used for cDNA synthesis  
 CC were complementary to the 5' end of the CHI domain of the heavy  
 CC chain expressed by the hybridoma of interest, or to the 5' end of  
 CC the C kappa domain. Some of the primers used for cDNA synthesis are  
 CC shown in 097511-097518. The primer used for cDNA synthesis of the  
 CC variable region of a particular antibody polypeptide was also used  
 CC for PCR amplification of that variable region. In conjunction with  
 CC an appropriate V-region primer. In addition, the VH primer 097518  
 CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences  
 CC of the PCR amplified nucleotides were determined. These are given  
 CC in 097498-097510 and the deduced AA sequences in R79241-R79250 &  
 CC R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45  
 CC and in the claims are different from the descriptions in the  
 CC sequence listings. The descriptions in the sequence listings are  
 CC used here.  
 SQ Sequence 107 AA;

Query Match 94.1%; Score 64; DB 14; Length 107;  
 Best Local Similarity 88.9%; Pred. No. 2.34e+01;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 79 esedfvay 87  
 |||||  
 99 ESEDFVAY 107

RESULT 4  
 ID R79247 standard; Protein; 107 AA.  
 AC R79247;  
 DE 21-DEC-1995 (first entry)  
 DE Light chain variable region for monoclonal antibody 1F10.  
 KM Monoclonal antibody; heavy metal; mercury; variable region;

KM light chain.  
 OS Synthetic.  
 PN MO9520607-A.  
 PD 03-AUG-1995.  
 PE 27-JAN-1995; U01199.  
 PR 27-JAN-1994; US-187407.  
 PA (BION-) BIONEBRASKA INC.  
 PI Lopez O, Wagner FW, Wylie DE;  
 DR WPI: 95-275415/36.  
 PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from  
 PT monoclonal antibodies, used for detecting, removing, adding or  
 PT neutralising heavy metals  
 PS Claim 23: Page 62: 106pp; English.  
 CC Hybridoma antibodies have been produced with the spleen cells of  
 CC BMB/c mouse that had received multiple injections of mercuric ions  
 CC reacted with glutathione to produce a mercuric ion coordinate  
 CC covalent compound which was covalently bound to keyhole limpet  
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,  
 CC 5B6 and 3E8) were producing Mabs that were strongly positive  
 CC against glutathione-mercuric ions but negative against glutathione  
 CC without mercuric ions. RNA was isolated from hybridoma cells with  
 CC by Mulv reverse transcriptase. First strand cDNA synthesis was catalysed  
 CC were complementary to the 5' end of the CHI domain of the heavy  
 CC chain expressed by the hybridoma of interest, or to the 5' and of  
 CC the C kappa domain. Some of the primers used for cDNA synthesis are  
 CC shown in Q97511-Q97518. The primer used for cDNA synthesis of the  
 CC variable region of a particular antibody polypeptide was also used  
 CC for PCR amplification of that variable region, in conjunction with  
 CC an appropriate V-region primer. In addition, the VH primer Q97518  
 CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences  
 CC of the PCR amplified nucleotides were determined. These are given  
 CC in Q97498-Q97510 and the deduced AA sequences in R79241-R79250 &  
 CC R8970-R8971. The descriptions of the SEQ ID nos given on pp 44-45  
 CC and in the claims are different from the descriptions in the  
 CC sequence listings. The descriptions in the sequence listings are  
 CC used here. 107 AA;  
 SQ Sequence 107 AA;

Query Match 94.1%; Score 64; DB 14; Length 107;  
 Best Local Similarity 88.9%; Pred. No. 2.34e+01;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 79 esedfvdvdy 87  
 ||||| ||  
 QY 99 ESEDFVAYY 107

RESULT 5  
 ID R79250 standard; Protein; 107 AA.  
 AC R79250;  
 DT 21-DEC-1995 (first entry)  
 DE Light chain variable region for monoclonal antibody 5G4.  
 KM Monoclonal antibody; heavy metal; mercury; variable region;  
 OS light chain.  
 OS Synthetic.  
 PN MO9520607-A.  
 PD 03-AUG-1995.  
 PE 27-JAN-1995; U01199.  
 PR 27-JAN-1994; US-187407.  
 PA (BION-) BIONEBRASKA INC.  
 PI Lopez O, Wagner FW, Wylie DE;  
 DR WPI: 95-275415/36.  
 PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from  
 PT monoclonal antibodies, used for detecting, removing, adding or  
 PT neutralising heavy metals  
 PS Claim 23: Page 66: 106pp; English.  
 CC Hybridoma antibodies have been produced with the spleen cells of  
 CC BMB/c mouse that had received multiple injections of mercuric ions  
 CC reacted with glutathione to produce a mercuric ion coordinate  
 CC covalent compound which was covalently bound to keyhole limpet

CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,  
 CC 5B6 and 3E8) were producing Mabs that were strongly positive  
 CC against glutathione-mercuric ions but negative against glutathione  
 CC without mercuric ions. RNA was isolated from hybridoma cells with  
 CC by Mulv reverse transcriptase. First strand cDNA synthesis was catalysed  
 CC were complementary to the 5' end of the CHI domain of the heavy  
 CC chain expressed by the hybridoma of interest, or to the 5' and of  
 CC the C kappa domain. Some of the primers used for cDNA synthesis are  
 CC shown in Q97511-Q97518. The primer used for cDNA synthesis of the  
 CC variable region of a particular antibody polypeptide was also used  
 CC for PCR amplification of that variable region, in conjunction with  
 CC an appropriate V-region primer. In addition, the VH primer Q97518  
 CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences  
 CC of the PCR amplified nucleotides were determined. These are given  
 CC in Q97498-Q97510 and the deduced AA sequences in R79241-R79250 &  
 CC R8970-R8971. The descriptions of the SEQ ID nos given on pp 44-45  
 CC and in the claims are different from the descriptions in the  
 CC sequence listings. The descriptions in the sequence listings are  
 CC used here. 107 AA;  
 SQ Sequence 107 AA;

Query Match 94.1%; Score 64; DB 14; Length 107;  
 Best Local Similarity 88.9%; Pred. No. 2.34e+01;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 79 esedfvdvdy 87  
 ||||| ||  
 QY 99 ESEDFVAYY 107

RESULT 6  
 ID R21310 standard; Protein; 108 AA.  
 AC R21310;  
 DT 21-MAY-1992 (first entry)  
 DE Light chain of Mif clone.  
 KM Fd: bacteriophage; gene III; filamentous; phagemid; capsid; coat;  
 KM plus; gfp; binding; adscription; gene VIII; diverse repertoire;  
 KM specific binding pairs; replicable genetic display package.  
 OS Synthetic.  
 OS Key  
 FT region 25..34  
 FT /label= CDR1  
 FT 50..56  
 FT /label= CDR2  
 FT 89..96  
 FT /label= CDR3  
 PN MO9201047-A.  
 PD 23-JAN-1992.  
 PE 10-JUL-1991; G01134.  
 PR 10-JUL-1990; GB-015198.  
 PR 19-OCT-1990; GB-022845.  
 PR 12-NOV-1990; GB-024503.  
 PR 06-MAR-1991; GB-004744.  
 PR 15-MAY-1991; GB-010549.  
 PA (CAMP-) CAMBRIDGE ANTIBODY.  
 PA (MEDT-) MED RES COUNCIL.  
 PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;  
 PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;  
 PI Winter GR, Bonnett TP;  
 DR WPI: 92-056862/07.  
 PT Producing members of specific binding pairs - by expression in  
 PT recombinant host cells with a secreting replicable genetic  
 PT display package.  
 PS Example 46: Fig 52: 109pp; English.  
 CC The sequence is the light chain of clone MJF encoding an scfv frag-  
 CC ment specific for both hen and turkey egg lysozyme (HEL and TRL).  
 CC The DNA encoding the chain was amplified from a cDNA library prep.  
 CC from the spleen of an unimmunised mouse. The corresponding heavy  
 CC chain was also amplified from an existing construct, pSV1-VHD1.3  
 CC (Ward et al, 1989). The two fragments were assembled via a linker  
 CC to prepare an scfv construct which was ligated into the fdCAT2  
 CC vector for expression on the surface of fd bacteriophage. In this

CC way, the VL domain was replaced by a library of VL domains to allow  
CC for selection of a broader range of antibody specificities. Several  
CC clones were isolated which bound to rIL (the parent antibody D1.3  
CC binds exclusively to HEL). The sequences of the light chains of  
CC two of these clones, M1 and M2 are given in R21310 and R21311  
CC respectively. The D1.3 light chain is given in R21309  
CC See also R21260-307, 309-312, R22450, R22565, R22567-81.  
SQ Sequence 108 AA;

Query Match 94.1%; Score 64; DB 4; Length 108;  
Best Local Similarity 88.9%; Pred. No. 2.34e+01;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 79 esedfvdy 87  
|||||  
OY 99 ESEDFVAY 107

SQUL 7  
P30251 standard; peptide: 146 AA.  
P30251:

DE 25-MAY-1992 (first entry)  
DE Sequence of the leader, variable region and first 16 AAs of  
DE the constant region of the kappa-chain (light chain) of MOPC41.  
KM Diagnosis; therapy; immunoglobulin.  
OS Homo sapiens.

FT Key Location/Qualifiers  
FT region 1..22  
FT /label= leader  
FT region 23..130  
FT /label= variable  
FT region 131..146  
FT /label= constant

PN EP--88994-A.  
PD 21-SEP-1983.  
PF 10-MAR-1983; 001655.  
PR 15-MAR-1982; US-358414.  
PR 05-DEC-1983; US-558551.  
PA (SCHE ) SCHERING CORP.  
PA (DNAX-) DNAX RES INST.  
PI Moore KW, Zalfaront A;  
DR WPI: 83-772290/39.  
DR N-PSDB: N30165.  
PT Transformed expression vectors or plasmid(s) - with double  
PT stranded DNA sequence coding only for desired part of polypeptide  
PT chain.  
Example: Page 40-41; 68pp; English.

CC The pref. vector or plasmid of the invention has a double-stranded  
CC DNA seq. coding for a variable region of a light or heavy chain of  
CC IgG, or for a variable region of a light or heavy chain of an  
CC immunoglobulin specific for an enzyme or surface protein. The  
CC sequence esp. codes for a variable region of a light chain having 95-  
CC 115 AAs or for a variable region of a heavy chain having 110-125 AAs  
CC esp. including the D region of the heavy chain.  
SQ Sequence 146 AA;

Query Match 94.1%; Score 64; DB 4; Length 146;  
Best Local Similarity 88.9%; Pred. No. 2.34e+01;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 101 esedfvdy 109  
|||||  
OY 99 ESEDFVAY 107

RESULT 8  
ID W02280 standard; Protein: 243 AA.  
AC W02280;

DE 29-OCT-1996 (first entry)  
DE 520C9 anti-c-erbB-2 two single chain Fv construct.  
KM 520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sfv;  
KM construct; polypeptide linker; C-terminal amino acid sequence;  
KM in vivo imaging; drug targeting experiment; homodimer;

KM increased; binding avidity; tissue retention time.  
OS Homo sapiens.

FT Key Location/Qualifiers  
FT peptide 118..133  
FT /label= linker

PN US5534254-A.  
PD 09-JUL-1996.  
PF 06-FEB-1992; 831967.  
PR 06-FEB-1992; US-831967.  
PR 07-OCT-1993; US-133804.  
PA (CHIR ) CHIRON CORP.  
PA (CREA-) CREATIVE BIOMOLECULES INC.  
PI Houston LT, Huston JS, Oppermann H, Ring DB;  
DR WPI: 96-333194/33.  
DR N-PSDB: T36880.

PT Compsns. contg. antigen-targeting antibody fragment constructs -  
PT comprising dimer of single-chain Fv fragments  
PS Example 1; Columns 33-36; 30pp; English.  
CC Variable heavy (VH) and variable light (VL) genes were cloned from  
CC a 520C9 hybridoma cDNA library, using probes directed toward the  
CC antibody constant and joining regions. A two single chain Fv (sfv)  
CC gene was constructed by connecting the VH and VL genes with a  
CC Ser rich polypeptide linker. The resulting 520C9 two sfv gene,  
CC which encodes the present sequence, was inserted into an expression  
CC vector, transformed into E. coli, and protein expression induced by  
CC the addn. of IPTG to the culture medium.  
CC A compsn. comprising a carrier and the 2 sfv protein prod. can be  
CC used for in vivo imaging, and drug targeting experiments. The  
CC 2 sfv protein prod. is a homodimer, in which both fragments target  
CC the same antigen, therefore giving greater binding avidity and  
CC longer tissue retention times, compared to individual sfv protein  
CC prod. fragments.  
SQ Sequence 243 AA;

Query Match 94.1%; Score 64; DB 18; Length 243;  
Best Local Similarity 88.9%; Pred. No. 2.34e+01;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 212 esedfvdy 220  
|||||  
OY 99 ESEDFVAY 107

RESULT 9  
ID R39569 standard; Protein: 246 AA.  
AC R39569;

DE 07-FEB-1994 (first entry)  
DE Sequence of 520C9 sfv protein.  
KM Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;  
KM biosynthetic single polypeptide chain binding site; ss.  
OS Synthetic.  
PN W09316185-A.  
PD 19-AUG-1993.  
PF 05-FEB-1993; 001055.  
PR 06-FEB-1992; US-831967.

PA (CETU ) CERUS ONCOLOGY CORP.  
PA (CREA-) CREATIVE BIOMOLECULES INC.  
PI Houston LT, Huston JS, Oppermann H, Ring DB;  
DR WPI: 93-272889/34.  
DR N-PSDB: Q46084.

PT New single chain Fv polypeptide binding to C-erbB-2 tumour  
PT antigen - for imaging or treating breast or ovarian cancer etc.  
PS Claim 4; pages 60-61; 87pp; English.  
CC C-erbB-2 refers to a protein antigen expressed on the surface of  
CC tumour cells, such as breast and ovarian tumour cells, which is an  
CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric  
CC pt. of about 5.3 (see Q46083, R39568). A single chain Fv (sfv)  
CC is a covalently linked VH-VL heterodimer which is expressed from  
CC a gene fusion including VH- and VL- encoding genes connected by  
CC a peptide-encoding linker. Such linker sequences are set forth in  
CC AA residues 116-135 in R39569, which includes part of the 16 AA  
CC linker sequences in R39572. Using Q46084 for the 520C9 monoclonal  
CC antibody, a single chain polypeptide can be produced having a

CC binding affinity for a c-erbB-2 related antigen. 'X' in R39569  
CC refers to the location of a stop codon in Q46084.  
SQ Sequence 246 AA.

Query Match 94.1%; Score 64; DB 8; Length 246;  
Best Local Similarity 88.9%; Pred. No. 2,34e+01;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 212 esedfvvay 220  
||| ||| ||  
QY 99 ESEDFVAY 107

RESULT 10  
ID R39571 standard; Protein: 534 AA.

AC R39571.  
DT 07-FEB-1994 (first entry)  
DE Sequence of G-FIT.  
SQ Tumour antigen; c-erbB-2; G-FIT.  
Synthetic.  
MO9316185-A.

PD 19-AUG-1993.  
PF 03-FEB-1993; U01055.  
PR 06-FEB-1992; US-831967.  
PA (CETU) CETUS ONCOLOGY CORP.  
PI (CREA-) CREATIVE BIOMOLECULES INC.  
PI Houston IL, Huston JS, Oppermann H, Ring DB;  
DR WPT: 93-272889/34.  
DR N-PSDB: Q46086.

PT New single chain Fv polypeptide binding to C-erbB-2 tumour  
PT antigen - for imaging or treating breast or ovarian cancer etc.  
PS Example; pages 65-68; 87pp; English.  
CC C-erbB-2 refers to a protein antigen expressed on the surface of  
CC tumour cells such as breast and ovarian tumour cells, which is an  
CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric  
CC pt. of about 5.3 (see Q46083, R39568).  
SQ Sequence 534 AA;

Query Match 94.1%; Score 64; DB 8; Length 534;  
Best Local Similarity 88.9%; Pred. No. 2,34e+01;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 503 esedfvvay 511  
||| ||| ||  
QY 99 ESEDFVAY 107

SUPL 11  
R92829 standard; Protein: 255 AA.

DT 09-MAY-1996 (first entry)  
DE C179FV-PP variable light chain sequence.  
KW Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;  
OS haemagglutinin; variable light chain; therapy.  
KS Synthetic.

FT Key Location/Qualifiers:  
FT protein 26..126  
FT domain /note="variable light chain"  
FT domain /note="Fc binding domain-like structure"  
FT domain /note="Fc binding domain-like structure"  
FT domain 194..251  
FT domain /note="Fc binding domain-like structure"

PN EP-675199-A2.

PD 04-OCT-1995.

PF 14-MAR-1995; 301664.

PR 30-MAR-1994; JP-082693.

PA (TAKI) TAKARA SHUZO CO LTD.

PI Atsushi O, Hirofumi Y, Ikunoshin K, Takashi T, Yoshinobu O;

DR N-PSDB: T04179.

DR Gene encoding variable region of anti-human influenza A type virus

PT antibody - useful for prodn. of artificial antibodies

PS Example 4; Page 33-35; 42pp; English

CC This sequence represents the variable light chain of C179FV-PP. The  
CC variable heavy chain sequence of C179FV-PP is shown in R92829. These  
CC sequences form an anti-human influenza A type virus antibody. The  
CC antibody recognises the stem region of the haemagglutinin (HA) molecule  
CC of the H1N1 and H2N2 subtypes of human influenza A type virus, and shows  
CC neutralisation activity against these two subtypes. The antibody shows  
CC no recognition of the H3N2 subtype. This sequence and the variable light  
CC chain coding sequence (see T04160) are useful in the production of  
CC artificial antibodies and antigen-binding polypeptides. These artificial  
CC antibodies and polypeptides are useful in the diagnosis and treatment of  
CC human influenza. As the antibodies recognise the stem region of the HA  
CC molecule, the influenza virus will be recognised even if the HA molecule  
CC changes. This provides an advantage over current vaccines, as the virus  
CC periodically alters its HA molecule.  
SQ Sequence 255 AA;

Query Match 89.7%; Score 61; DB 16; Length 255;  
Best Local Similarity 66.7%; Pred. No. 4,22e+01;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 101 gnedfvay 109  
::: ||| ||| ||  
QY 99 ESEDFVAY 107

RESULT 12  
ID R82835 standard; Protein: 392 AA.

AC R82835.  
DT 09-MAY-1996 (first entry)  
DE scfv-pp.  
KW Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;  
KW haemagglutinin; variable heavy chain; therapy.  
OS Synthetic.

FT Key Location/Qualifiers:  
FT protein 23..144  
FT protein /note="variable heavy chain"  
FT protein 164..263  
FT protein /note="variable light chain"  
FT domain 273..330  
FT domain /note="Fc binding domain-like structure"  
FT domain 331..388  
FT domain /note="Fc binding domain-like structure"

PN EP-675199-A2.  
PD 04-OCT-1995.  
PF 14-MAR-1995; 301664.  
PR 30-MAR-1994; JP-082693.  
PA (TAKI) TAKARA SHUZO CO LTD.  
PI Atsushi O, Hirofumi Y, Ikunoshin K, Takashi T, Yoshinobu O;  
DR N-PSDB: T04180.

PT Gene encoding variable region of anti-human influenza A type virus  
PT antibody - useful for prodn. of artificial antibodies  
PS Example 4; Page 36-38; 42pp; English.  
CC This sequence represents the scfv-pp fusion polypeptide. This sequence  
CC is an anti-human influenza A type virus antibody. The antibody  
CC recognises the stem region of the haemagglutinin (HA) molecule of the  
CC H1N1 and H2N2 subtypes of human influenza A type virus, and shows  
CC neutralisation activity against these two subtypes. The antibody shows  
CC no recognition of the H3N2 subtype. Artificial antibodies (such as this)  
CC and polypeptides are useful in the diagnosis and treatment of human  
CC influenza. As the antibodies recognise the stem region of the HA  
CC molecule, the influenza virus will be recognised even if the HA molecule  
CC changes. This provides an advantage over current vaccines, as the virus  
CC periodically alters its HA molecule.  
SQ Sequence 392 AA;

Query Match 89.7%; Score 61; DB 16; Length 392;  
Best Local Similarity 66.7%; Pred. No. 4,22e+01;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 238 gnedfvay 246  
::: ||| ||| ||  
QY 99 ESEDFVAY 107

ID	RESULT	13
AC	R82826: standard; Protein; 98 AA.	
DT	08-MAY-1996 (first entry)	
DE	Variable light region of the anti-human influenza A type virus antibody.	
KW	Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;	
OS	haemagglutinin; variable heavy chain; therapy.	
OS	Mus musculus.	
FT	Key	Location/Qualifiers
FT	region	28..33
FT	region	/label= CDR1
FT	region	50..55
FT	region	/label= CDR2
FT	region	90..94
FT	region	/label= CDR3
PN	EP-675199-A2.	
PN	04-OCT-1995.	
PN	14-MAR-1995; 301664.	
PN	30-MAR-1994; JP-0826693.	
PA	(TAKI) TAKARA SHUZO CO LTD.	
PA	Atsushi O, Hirofumi Y, Ikunoshin K, Takashi T, Yoshinobu O;	
DR	WPI: 95-338286/44.	
DR	N-PSDB: T04160.	
PT	Gene encoding variable region of anti-human influenza A type virus	
PT	antibody - useful for prodn. of artificial antibodies	
PS	Claim 2; Page 20; 42pp; English.	
CC	This sequence represents the variable heavy chain region of an anti-human	
CC	influenza A type virus antibody. The antibody recognises the stem region	
CC	of the haemagglutinin (HA) molecule of the H1N1 and H2N2 subtypes of	
CC	human influenza A type virus, and shows neutralisation activity against	
CC	these two subtypes. The antibody shows no recognition of the H3N2	
CC	subtype. The DNA encoding this sequence and the variable heavy chain	
CC	coding sequence (see T04159) are useful in the production of artificial	
CC	antibodies and antigen-binding polypeptides. These artificial antibodies	
CC	and polypeptides are useful in the diagnosis and treatment of human	
CC	influenza. As the antibodies recognise the stem region of the HA	
CC	molecule, the influenza virus will be recognised even if the HA molecule	
CC	changes. This provides an advantage over current vaccines, as the virus	
CC	periodically alters its HA molecule.	
SC	Sequence 98 AA;	

Query Match	85.3%;	Score 58;	DB 16;	Length 98;
Best Local Similarity	55.6%;	Pred. No. 7.56e+01;		
Matches	5;	Conservative	4;	Mismatches 0;
				Indels 0;
				Gaps 0;

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79 qaqqdfvsyy 87
  ::::|::|
QY 99 ESEDFVAYY 107

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ID	RESULT	14
AC	R80079; standard; Protein; 90 AA.	
DI	22-MAY-1996 (first entry),	
DE	Mouse derived light chain R13 phage antibody pattern C.	
DE	Light chain; R13; murine; catalytic antibody; bacteriophage;	
KW	pattern C.	
OS	Mus musculus.	
FH	Key	
FT	region	Location/Qualifiers
FT	region	1..15
FT	region	/note- "framework region 1"
FT	region	16..26
FT	region	/note- "complementarity determining region 1"
FT	region	27..40
FT	region	/note- "framework region 2"
FT	region	41..47
FT	region	/note- "complementarity determining region 2"
FT	region	48..78
FT	region	/note- "framework region 3"
FT	region	79..88
FT	region	/note- "complementarity determining region 3"

FT	region	89..90	/note="framework region 4
FT			N-terminal fragment"
PD	W09527045.A1.		
PD	12-OCT-1995.		
PF	30-MAR-1994;	W03420.	
PR	30-MAR-1994;	UO-003420.	
PA	(IGEN- )	IGEN INC.	
PI	Chiswell, D.	Darsley MJ, Fitzgerald K, Kenten JH.	
PI	Malin MW, Mcclerety J, Smith RG, Tilmans RC, Williams RO.		
DR	WPI: 95-358624/46.		
DR	N-PSDS: T04626.		
PT	Production of catalytic antibodies displayed on phage - by		
PT	generating a gene library of antibody-derived domains and expressing		
PT	it in phage vectors		
PS	Disclosure; Fig 9; 133pp. English.		
CC	T04626 encodes R80079 mouse derived light chain R73 phage antibody.		
CC	The DNA was used in the prepn. of catalytic antibody (CA) producing		
CC	bacteriophage. The CAs can be used to activate/deactivate a		
CC	biological function in an animal by enhancing the rate of cleavage,		
CC	or formation of a specific bond within a mol. in vivo.		
SQ	Sequence 90 Aa;		

Query Match	83.8%	Score 57	DB 16	length 90
Best Local Similarity	77.8%	Pred. No.	9.17e+01	
Matches	7	Conservative	0	Mismatches 2
			Indels	0
			Gaps	0
Db	69 esedfady	77		
Oy	99 ESEDFVAY	107		

ID	W31726	standard:	peptide: 107 AA.
AC	W31726:		
DT	29-APR-1998	(first entry)	
DE	Alpha light chain amino acid sequence of the Fab molecule clone I1.		
CC	Alpha light chain; Fab molecule; binding; hepatitis C virus; HCV;		
KW	E2 antigen; combinatorial antibody library; vaccine; antibody;		
KM	recombinant human monoclonal antibody; immunological binding affinity;		
OS	passive immunity.		
FS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	Region	23..34	
FT		/note= "CDR 1"	
FT	Region	50..56	
FT		/note= "CDR 2"	
FT	Region	89..97	
FT		/note= "CDR 3"	
PN	MO9740176-A1.		
PD	30-OCT-1997.		
PF	18-APR-1997; E01977.		
PR	17-APR-1997; US-844215.		
PR	19-APR-1996; US-635109.		
PA	(ALIA/) ALLANDER T E.		
PA	(PERS/) PERSSON M A.		
PI	Allander TE, Persson MA;		
DR	WPI: 97-535657/49.		
DR	N-PSDB: T88837.		
PT	New human monoclonal antibodies to hepatitis C virus E2 antigen -		
PT	obtained using a combinatorial antibody library prepared using RNA		
PT	from a HCV infected subject, useful for vaccine preparation		
PS	Claim 5: Fig 2E: 103pp, English.		
CC	The present sequence represents the alpha light chain peptide sequence		
CC	of the Fab molecule, clone I1. This immunoglobulin molecule is		
CC	capable of specifically binding with the hepatitis C virus (HCV)		
CC	E2 antigen. The present sequence was obtained from a combinatorial		
CC	antibody library. The alpha light chain peptide can be used to construct		
CC	a recombinant human monoclonal antibody (Mab). The monoclonal antibodies		
CC	exhibit immunological binding affinity for HCV E2 antigen and are		
CC	cross-reactive with different HCV strains. They can be used to produce		
CC	vaccine compositions which can be used to provide antibodies to HCV in		
CC	a subject or to provide passive immunity or to treat HCV infected		



CC subjects. They can also be used to detect HCV and to monitor anti-HCV  
CC therapeutic treatment.  
CC note: this sequence is allegedly encoded by T8837; however, the  
CC peptide encoded by that nucleotide sequence differs considerably to the  
CC present peptide.  
SQ Sequence 107 AA;

Query Match 83.8%; Score 57; DB 28; Length 107;  
Best local Similarity 77.8%; Pred. No. 9.17e+01;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 79 esedfavy 87  
|||  
OY 99 ESEDFVAY 107

Search completed: Tue Apr 20 14:01:59 1999  
Job time : 16 secs.

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D.: Marshak-Rothstein, A.; Weigert, M.  
J. Exp. Med. (1990) 171:265-297  
Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.  
#cross-references MIMD:90111618  
#accession PLO260  
#molecule-type mRNA  
#residues 1-106 #label SHL  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotrimer; immunoglobulin  
FEATURE  
1-23 #region framework 1\  
24-34 #region complementarity-determining 1\  
35-49 #region framework 2\  
50-56 #region complementarity-determining 2\  
57-88 #region framework 3\  
89-97 #region complementarity-determining 3\  
98-106 #region framework 4  
#length 106 #checksum 2157

Query Match 94.1%; Score 64; DB 2; Length 106;  
Best Local Similarity 88.9%; Pred. No. 4,48e-01;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 79 ESEDFVDY 87  
QY 99 ESEDFVAY 107

RESULT 3  
ENTRY PLO259 #type fragment  
TITLE Ig kappa chain V region (anti-DNA, DP1YK) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
REFERENCE PLO259  
#authors Shlomchik, M.; Mascello, M.; Shan, H.; Radic, M.Z.; Plisetsky, D.; Marshak-Rothstein, A.; Weigert, M.  
#journal J. Exp. Med. (1990) 171:265-297  
#title Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.  
#cross-references MIMD:90111618  
#accession PLO259  
#molecule-type mRNA  
#residues 1-106 #label SHL  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotrimer; immunoglobulin  
FEATURE  
1-23 #region framework 1\  
24-34 #region complementarity-determining 1\  
35-49 #region framework 2\  
50-56 #region complementarity-determining 2\  
57-88 #region framework 3\  
89-97 #region complementarity-determining 3\  
98-106 #region framework 4  
#length 106 #checksum 2162

Query Match 94.1%; Score 64; DB 2; Length 106;  
Best Local Similarity 88.9%; Pred. No. 4,48e-01;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 79 ESEDFVDY 87  
QY 99 ESEDFVAY 107

RESULT 4  
ENTRY RYMSM4 #type complete  
TITLE Ig kappa chain precursor V region (MOPC 41) - mouse  
CONTAINS Ig kappa chain precursor V region VK41  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change

16-Aug-1996  
ACCESSIONS A93211; B93211; A93815; A94239; A01922; A01923  
REFERENCE A93211  
#authors Seidman, J.G.; Max, E.E.; Leder, P.  
#journal Nature (1979) 280:370-375  
#title A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.  
#cross-references MIMD:79221900  
#accession A93211  
#molecule-type DNA  
#residues 1-130 #label PC41  
#accession B93211  
#molecule-type DNA  
#residues 1-117 #label VK41  
#note the sequences were determined from the differentiated gene MOPC 41 and the germ-line gene VK41

REFERENCE A93815  
#authors Bursstein, Y.; Schechter, I.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720  
#title Amino acid sequence of the NH-2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda-1-type and kappa-type light chains.  
#cross-references MIMD:77148916  
#accession A93815  
#molecule-type protein  
#residues 1-33 #label BUR  
#note Met-3 is apparently used as an alternative initiator in 25% of the chains

REFERENCE A94239  
#authors Gray, W.R.; Dreyer, W.J.; Hood, L.  
#journal Science (1967) 155:465-467  
#title Mechanism of antibody synthesis: size differences between mouse kappa chains.  
#cross-references MIMD:67056897  
#accession A94239  
#molecule-type protein  
#residues 23-49, 'B', '51-53', 'LSB', '57-58', '72', '61-62', 'B2', '65-76', 'B', '78-108, 110-130 #label GRA  
#note ##experimental\_source Bence Jones protein MOPC 41

GENETICS 19/1  
#introns An immunoglobulin heterotrimer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into larger oligomers.  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS alternative initiators; heterotrimer; immunoglobulin  
FEATURE  
1-72 #domain signal sequence #status experimental #label SIG1\  
73-72 #domain signal sequence #status experimental #label SIG2\  
23-130 #product Ig kappa chain V region (MOPC 41) #status experimental #label M41\  
38-112 #domain immunoglobulin homology #label IMM\  
45-110 #disulfide\_bonds #status predicted  
SUMMARY #length 130 #molecular\_weight 14311 #checksum 6707

Query Match 94.1%; Score 64; DB 1; Length 130;  
Best Local Similarity 88.9%; Pred. No. 4,48e-01;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 101 ESEDFVDY 109  
QY 99 ESEDFVAY 107

RESULT 5  
ENTRY H30502 #type complete  
TITLE Ig kappa chain V region (D42) - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 03-Nov-1988 #sequence\_revision 03-Aug-1992 #text\_change  
20-Mar-1998

ACCESSIONS H30502  
REFERENCE A30502  
#authors Eliat, D.; Webster, D.M.; Rees, A.R.  
#journal J. Immunol. (1988) 141:1745-1753  
#title V region sequences of anti-DNA and anti-RNA autoantibodies  
from NZB/NZW F-1 mice.  
#cross-references M01D:88315787  
#accession H30502  
#status Preliminary  
#molecule\_type mRNA  
#residues 1-103 #label ETL  
#cross-references GB:M21912; NID:9197077; PID:9197078  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SUMMARY #length 103 #molecular\_weight 11280 #checksum 1572

Query Match 89.7%; Score 61; DB 2; Length 103;  
Best Local Similarity 77.8%; Pred. No. 1.48e+00;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 76 EPEDEVY 84  
||| ||| ||  
QY 99 ESEDFVAY 107

RESULT 6  
ENTRY F30607 #type fragment  
TITLE Ig kappa chain V-II region (Bor) - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change  
16-Aug-1996

ACCESSIONS F30607  
REFERENCE A30601  
#authors Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;  
Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;  
Frangione, B.  
#journal J. Immunol. (1989) 142:3158-3163  
#title Structural and idiotypic characterization of the L chains of  
human IgM autoantibodies with different specificities.  
#cross-references M01D:89215279  
#accession F30607  
#status Preliminary  
#molecule\_type protein  
#residues 1-109 #label GON  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SUMMARY #length 109 #checksum 6514

Query Match 89.7%; Score 61; DB 2; Length 109;  
Best Local Similarity 77.8%; Pred. No. 1.48e+00;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 80 EPEDEVY 88  
||| ||| ||  
QY 99 ESEDFVAY 107

RESULT 7  
ENTRY S37510 #type fragment  
TITLE Ig kappa chain V region (V-kappa 3) - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change  
08-Sep-1997

ACCESSIONS S37501  
REFERENCE S37501  
#authors Klein, U.; Kuipers, R.; Rajewsky, K.  
#submission Submitted to the EMBL Data Library, September 1993  
#description Human IgM(+)IgD(+) cells, the major B cell subset in the  
peripheral blood, expresses V(kappa) genes with no or  
little somatic mutation throughout life.  
#accession S37510

#status Preliminary  
#molecule\_type mRNA  
#residues 1-92 #label KLE  
#cross-references EMBL:226601; NID:9405662; PID:9405663  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SUMMARY #length 92 #checksum 6347

Query Match 85.3%; Score 58; DB 2; Length 92;  
Best Local Similarity 66.7%; Pred. No. 4.74e+00;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 63 QPEDEVY 71  
||| ||| ||  
QY 99 ESEDFVAY 107

RESULT 8  
ENTRY S17622 #type complete  
TITLE Ig kappa chain V region - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change  
09-May-1997

ACCESSIONS S17622  
REFERENCE S17230  
#authors Clarkson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
#journal Nature (1991) 352:624-628  
#title Making antibody fragments using phage display libraries.  
#cross-references M01D:91326098  
#accession S17622  
#status Preliminary  
#molecule\_type nucleic acid  
#residues 1-91 #label CLA  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SUMMARY #length 91 #molecular\_weight 9895 #checksum 3446

Query Match 83.8%; Score 57; DB 2; Length 91;  
Best Local Similarity 77.8%; Pred. No. 6.94e+00;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 71 ESEDFADY 79  
||| ||| ||  
QY 99 ESEDFVAY 107

RESULT 9  
ENTRY PH1062 #type fragment  
TITLE Ig light chain V region (clone 202.105) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change  
15-Jun-1996

ACCESSIONS PH1062  
REFERENCE PH0971  
#authors Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
#journal J. Exp. Med. (1992) 176:761-779  
#title Both IgM and IgG anti-DNA antibodies are the products of  
clonally selective B cell stimulation in (NZB x NZW)F1  
mice.  
#accession PH1062  
#status Preliminary  
#molecule\_type nucleic acid  
#residues 1-98 #label TIL  
#cross-references EMBL:226601; NID:9405662; PID:9405663  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
SUMMARY #length 98 #checksum 6933

Query Match 83.8%; Score 57; DB 2; Length 98;  
Best Local Similarity 77.8%; Pred. No. 6.94e+00;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 79 ESEDFADY 87

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OY      99 ESEDFVAY 107

RESULT  10
ENTRY   B28840 #type fragment
TITLE   Ig kappa chain V region (HP27) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change
        16-Aug-1996
ACCESSIONS #B28840; I25114
REFERENCE   A91028
#authors   Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau,
#journal   M.
#title     EMBO J. (1985) 4:3681-3688
#cross-references MUID:86136012
#accession   B28840
#molecule_type mRNA
#residues   1-101 #label OLL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY    #length 101 #checksum 7015

Query Match      83.8%; Score 57; DB 2; Length 101;
Best Local Similarity 77.8%; Pred. No. 6.94e+00;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db      73 ESEDFADY 81
OY      99 ESEDFVAY 107

RESULT  11
ENTRY   PL0262 #type fragment
TITLE   Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
        16-Aug-1996
ACCESSIONS #PL0262
REFERENCE   PL0231
#authors   Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
#journal   D.; Marshak-Rothstein, A.; Weigert, M.
#title     J. Exp. Med. (1990) 171:265-297
#cross-references MUID:90111618
#accession   PL0262
#molecule_type mRNA
#residues   1-106 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY    #region framework 1\
            #region complementarity-determining 1\
            #region framework 2\
            #region complementarity-determining 2\
            #region framework 3\
            #region complementarity-determining 3\
            #region framework 4
            #length 106 #checksum 658

Query Match      83.8%; Score 57; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 6.94e+00;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db      79 ESEDFADY 87
OY      99 ESEDFVAY 107

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RESULT  12
ENTRY   B47271 #type fragment
TITLE   nitrophenyl phosphonate-specific antibody 46G7 light chain VJ
ORGANISM #note
        - synthetic (fragment)
        #formal_name synthetic
        Mus musculus (house mouse) gene engineered and expressed in
        Escherichia coli
DATE     21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change
        11-Aug-1995
ACCESSIONS #B47271
REFERENCE   A47271
#authors   Lesley, S.A.; Patten, P.A.; Schultz, P.G.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1160-1165
#title     A genetic approach to the generation of antibodies with
#cross-references MUID:93165660
#accession   B47271
#molecule_type DNA; protein
#residues   1-108 #label LES
#note       sequence extracted from NCBI backbone (NCBIN:124856,
        NCBI:P:124859)
        parts of this sequence were determined by protein
        sequencing

FEATURE    24-89
SUMMARY    #disulfide_bonds #status predicted
            #length 108 #checksum 9036

Query Match      83.8%; Score 57; DB 4; Length 108;
Best Local Similarity 77.8%; Pred. No. 6.94e+00;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db      80 ESEDFADY 88
OY      99 ESEDFVAY 107

RESULT  13
ENTRY   KVM3B #type complete
TITLE   Ig kappa chain precursor V region (VKM173b) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change
        20-Mar-1998
ACCESSIONS #A01924
REFERENCE   A01924
#authors   Max, E.E.; Seidman, J.G.; Miller, H.; Leder, P.
#journal   Cell (1980) 21:793-799
#title     Variation in the crossover point of kappa immunoglobulin gene
#cross-references MUID:81064681
#accession   A01924
#molecule_type DNA
#residues   1-117 #label MAX
#cross-references GB:K00880; NID:g197443; PID:g197444
#note       the sequence was determined from the germline gene

GENETICS   19/1
#introns   An immunoglobulin heterotetramer subunit consists of two
            identical light (kappa or lambda) and two identical heavy
            (alpha, delta, epsilon, gamma, or mu) chains usually
            stabilized by interchain disulfide bonds. In some cases,
            such as IgA and IgM, the subunits associate into larger
            oligomers.

COMPLEX    #superfamily immunoglobulin V region; immunoglobulin homology
            heterotetramer

KEYWORDS   #domain signal sequence #status predicted #label SIG\
            #product Ig kappa chain V region (VKM173b) #status
            #disulfide_bonds #status predicted
            #length 117 #molecular_weight 12954 #checksum 3822

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer
FEATURE    1-22
SUMMARY    23-117
            45-110
            45-110

Query Match      83.8%; Score 57; DB 1; Length 117;
Best Local Similarity 77.8%; Pred. No. 6.94e+00;

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Matches 7: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 101 ESEDFADYY 109

QY 99 ESEDFVAYY 107

RESULT 14

ENTRY D32513 #type complete

TITLE Ig kappa chain precursor V region (BXW16) - mouse

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 20-Mar-1998

ACCESSIONS D32513

REFERENCE A94689

#authors Kotler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos, A.N.

#journal J. Clin. Invest. (1988) 82:852-860

#title Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice.

#cross-references MVID:8831394

#accession D32513

#molecule\_type DNA

#residues 1-129 #label KOF

#cross-references GB:M20832; NID:g196941; PID:g196942

CLASSIFICATION #superfamily Immunoglobulin V region; Immunoglobulin homology

KEYWORDS heterotetramer; Immunoglobulin

SUMMARY #length 129 #molecular-weight 14097 #checksum 3457

Query Match 83.8%; Score 57; DB 2; Length 129;

Best Local Similarity 77.8%; Pred. No. 6.94e+00;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 101 ESEDFADYY 109

QY 99 ESEDFVAYY 107

RESULT 15

ENTRY S34090 #type complete

TITLE Ig kappa chain V region - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-May-1997

ACCESSIONS S34090

REFERENCE S34076

#authors Wagner, S.D.; Luzatto, L.

#journal Eur. J. Immunol. (1993) 23:391-397

#title V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V-kappa locus and do not show somatic mutation.

#accession S34090

#status preliminary

#molecule\_type DNA

#residues 1-82 #label WAG

CLASSIFICATION #cross-references EMBL:X67174

KEYWORDS #superfamily Immunoglobulin V region; Immunoglobulin homology

SUMMARY heterotetramer; Immunoglobulin

#length 82 #molecular-weight 8891 #checksum 4385

Query Match 82.4%; Score 56; DB 2; Length 82;

Best Local Similarity 66.7%; Pred. No. 1.01e+01;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 70 QSEDFATYY 78

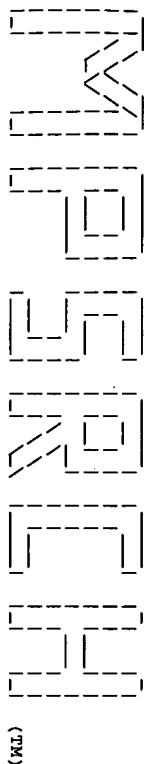
QY 99 ESEDFVAYY 107

Search completed: Tue Apr 20 14:01:25 1999

Job time : 18 secs.

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm  
on: Tue Apr 20 13:59:47 1999; Maspar time 2.35 Seconds  
Tabular output not generated. 102.676 Million cell updates/sec

Title: >US-08-836-455-2  
Description: (99-107) from US0836455.pep (3 of 3)  
Perfect Score: 68

Sequence: 1 ESEDPVAVY 9

Scoring table: PAM 150  
Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot35  
1:swissprot

Statistics: Mean 25.463; Variance 33.115; scale 0.769

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

sult	Query	Match	Length	DB	ID	Description	Pred. No.
No.	Score						
1	64	94.1	130	1	KV5G_MOUSE	IG KAPPA CHAIN PRECURS	3.87e-02
2	57	83.8	117	1	KV5H_MOUSE	IG KAPPA CHAIN PRECURS	1.05e+00
3	56	82.4	108	1	KV1K_HUMAN	IG KAPPA CHAIN V-I REG	1.65e+00
4	56	82.4	108	1	KV1N_HUMAN	IG KAPPA CHAIN V-I REG	1.65e+00
5	56	82.4	613	1	UI06_EBV	VIRION PROTEIN BBRI1	2.58e+00
6	55	80.9	107	1	KV1D_HUMAN	IG KAPPA CHAIN V-I REG	4.01e+00
7	54	79.4	100	1	KV3Q_HUMAN	IG KAPPA CHAIN PRECURS	4.01e+00
8	54	79.4	108	1	KV3A_HUMAN	IG KAPPA CHAIN V-III R	4.01e+00
9	54	79.4	109	1	KV3F_HUMAN	IG KAPPA CHAIN V-III R	4.01e+00
10	54	79.4	109	1	KV3D_HUMAN	IG KAPPA CHAIN V-III R	4.01e+00
11	54	79.4	109	1	KV3E_HUMAN	IG KAPPA CHAIN V-III R	4.01e+00
12	54	79.4	109	1	KV3G_HUMAN	IG KAPPA CHAIN V-III R	4.01e+00
13	54	79.4	112	1	KV1U_HUMAN	IG KAPPA CHAIN V-I REG	4.01e+00
14	54	79.4	115	1	KV3I_HUMAN	IG KAPPA CHAIN PRECURS	4.01e+00
15	54	79.4	128	1	KV3K_HUMAN	IG KAPPA CHAIN PRECURS	4.01e+00
16	54	79.4	129	1	KV3L_HUMAN	IG KAPPA CHAIN PRECURS	4.01e+00
17	54	79.4	129	1	KV3J_HUMAN	IG KAPPA CHAIN PRECURS	4.01e+00
18	53	77.9	108	1	KV1C_HUMAN	IG KAPPA CHAIN V-I REG	6.19e+00
19	53	77.9	108	1	KV1G_HUMAN	IG KAPPA CHAIN V-I REG	6.19e+00
20	53	77.9	108	1	KV1H_HUMAN	IG KAPPA CHAIN V-I REG	6.19e+00
21	53	77.9	108	1	KV1V_HUMAN	IG KAPPA CHAIN V-I REG	6.19e+00
22	53	77.9	108	1	KV1R_HUMAN	IG KAPPA CHAIN V-I REG	6.19e+00
23	53	77.9	109	1	KV3B_HUMAN	IG KAPPA CHAIN V-III R	6.19e+00

24	53	77.9	117	1	KV1I_HUMAN	IG KAPPA CHAIN PRECURS	6.19e+00
25	53	77.9	129	1	KV1X_HUMAN	IG KAPPA CHAIN PRECURS	6.19e+00
26	53	77.9	578	1	YEAF_ECOLI	HYPOTHETICAL 64.5 KD P	6.19e+00
27	53	77.9	901	1	VEF_GVTN	VITAL ENHANCING FACTOR	6.19e+00
28	53	77.9	901	1	VEF_GVPU	VITAL ENHANCING FACTOR	6.19e+00
29	52	76.5	108	1	KV1I_HUMAN	IG KAPPA CHAIN V-I REG	9.51e+00
30	52	76.5	108	1	KV1F_HUMAN	IG KAPPA CHAIN V-I REG	9.51e+00
31	52	76.5	109	1	KV1T_HUMAN	IG KAPPA CHAIN V-I REG	9.51e+00
32	52	76.5	117	1	KV1J_HUMAN	IG KAPPA CHAIN PRECURS	9.51e+00
33	52	76.5	259	1	IF2C_CYCA	TRANSLATION INITIATION	9.51e+00
34	52	76.5	715	1	ADSV_MOUSE	ADSEVERIN (GELSOLIN-LI	9.51e+00
35	52	76.5	715	1	ADSV_BOVIN	ADSEVERIN (SCINDERIN)	9.51e+00
36	51	75.0	116	1	KV3J_HUMAN	IG KAPPA CHAIN PRECURS	1.45e+01
37	51	75.0	408	1	KJ95_YEAST	HYPOTHETICAL 45.1 KD P	1.45e+01
38	50	73.5	108	1	KV5D_MOUSE	IG KAPPA CHAIN V-V REG	2.20e+01
39	50	73.5	108	1	KV1E_HUMAN	IG KAPPA CHAIN V-I REG	2.20e+01
40	50	73.5	115	1	KV3C_MOUSE	IG KAPPA CHAIN PRECURS	2.20e+01
41	50	73.5	426	1	ENO_HELPY	ENOLASE (EC 4.2.1.11)	2.20e+01
42	50	73.5	510	1	BAGT_MOUSE	BETA-1,4 N-ACETYLGLAC	2.20e+01
43	50	73.5	983	1	CAPR_ECOLI	PHOSPHOENOLPYRUVATE CA	2.20e+01
44	50	73.5	936	1	CAPR_RHOA	PHOSPHOENOLPYRUVATE CA	2.20e+01
45	50	73.5	1004	1	YD83_SCAPO	HYPOTHETICAL 112.0 KD	2.20e+01

## ALIGNMENTS

RESULT	1	STANDARD;	PRT;	130 AA.
ID	KV5G_MOUSE	P01639; P01640;		
AC	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 41).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
LN	EUTHERIA; RODENTIA.			
RX	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 79221900.			
RA	SEIDMAN J.G., MAX E.E., LEDER P.;			
RL	NATURE 280:370-375(1979).			
RN	[2]			
RP	SEQUENCE OF 1-33.			
RX	MEDLINE: 77148916.			
RA	BURSTEIN Y., SCHECHTER I.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 74:716-720(1977).			
RN	[3]			
RP	SEQUENCE OF 23-130.			
RX	MEDLINE: 67056897.			
RA	GRAY W.R., DREYER W.J., HOOD L.;			
RL	SCIENCE 155:465-467(1967).			
CC	- THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE SYSTEM DIRECTED BY			
CC	MRNA ISOLATED FROM MYELOMA POLYSOMES.			
CC	- THIS IS A BENGE-JONES PROTEIN.			
DR	PIR: A01922; KYMSM4.			
DR	HSP: P01607; 6FAB.			
KW	IMMUNOGLOBULIN V REGION; SIGNAL; BENGE-JONES PROTEIN.			
FT	SIGNAL	1	22	
FT	CHAIN	23	116	
FT	DOMAIN	23	45	
FT	DOMAIN	46	56	
FT	DOMAIN	57	71	
FT	DOMAIN	72	78	
FT	DOMAIN	79	110	
FT	DOMAIN	111	119	
FT	DOMAIN	120	129	
FT	DOMAIN	121	130	
FT	VARIANT	1	2	
FT	DISULFID	45	110	
FT	NON_TER	130	130	
SO	SEQUENCE	130 AA;	14311 MM;	E77D75A2 CRC32:
Query Match		94.1%;	Score 64;	DB 1; Length 130;
Best Local Similarity		88.9%;	Pred. No. 3.	87e-02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 101 ESEDFADY 109  
 |||||  
 QY 99 ESEDFVAY 107

RESULT 2  
 ID KVSJ\_MOUSE STANDARD; PRT: 117 AA.

AC P01641: 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 173B).  
 OS MUS MUSCULUS (MOUSE).  
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; RODENTIA.  
 RN [1]

SEQUENCE FROM N.A.  
 MEDLINE: 81064681.  
 MAX E.E., SEIDMAN J.G., MILLER H., LEDER P.;  
 RL CELL 21:793-799(1980).  
 DR EMBL; K00880; G197444; -.  
 DR PIR; A01924; KVM53B.  
 DR HSSP; P01607; IEGV.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT CHAIN 1 22  
 FT SIGNAL 23 117  
 FT DOMAIN 23 45  
 FT DOMAIN 46 56  
 FT DOMAIN 57 71  
 FT DOMAIN 72 78  
 FT DOMAIN 79 110  
 FT DOMAIN 111 >117  
 FT DISULFID 45 110  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12954 MW; 38F2E08C CRC32;

Query Match  
 Best Local Similarity 77.8%; Score 57; DB 1; Length 117;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 101 ESEDFADY 109  
 |||||  
 QY 99 ESEDFVAY 107

LT 3  
 KVIK\_HUMAN STANDARD; PRT: 108 AA.  
 AC P01603: 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-I REGION (KA).  
 OS HOMO SAPIENS (HUMAN).  
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; PRIMATES.  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE: 76189985.  
 RA SHINODA T.;  
 RL J. BIOCHEM. 77:1277-1296(1975).  
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC PIR; A01869; KIHOKA.  
 DR HSSP; P01607; IIGM.  
 KW IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN.

FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FRAMEWORK 1.  
 COMPLEMENTARITY-DETERMINING 1.  
 FRAMEWORK 2.  
 COMPLEMENTARITY-DETERMINING 2.  
 FRAMEWORK 3.  
 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11900 MW; 41BC730E CRC32;

Query Match  
 Best Local Similarity 82.4%; Score 56; DB 1; Length 108;  
 Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 79 ZPZBFATY 87  
 : : : : :  
 QY 99 ESEDFVAY 107

RESULT 4  
 ID KVIN\_HUMAN STANDARD; PRT: 108 AA.

AC P01606: 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-I REGION (OU).  
 OS HOMO SAPIENS (HUMAN).  
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; PRIMATES.  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE: 70201507.  
 RL KOHLER H., SHIMIZU A., PAUL C., PUTNAM F.W.;  
 SCIENCE 169:56-59(1970).  
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC PIR; A01872; KIHOUU.  
 DR HSSP; P01607; 2EGW.  
 KW IMMUNOGLOBULIN V REGION.

FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11777 MW; 4B089785 CRC32;

Query Match  
 Best Local Similarity 82.4%; Score 56; DB 1; Length 108;  
 Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 79 ZPZBFATY 87  
 : : : : :  
 QY 99 ESEDFVAY 107

RESULT 5  
 ID UL06\_EBV STANDARD; PRT: 613 AA.

AC P03213: 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)  
 DE VIRION PROTEIN BBRL.  
 GN BBRL.  
 OS EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
 CC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; GAMMAHERPESVIRINAE.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE: 84270667.  
 RA BAER R., BANKIER A.T., BIGGIN M.D., DEININGER P.L., FARRELL P.J.,  
 RA GIBSON T.J., HATFIELD G., HUDSON G.S., SATCHELL S.C., SEGGIN C.,  
 RA TURNER P.S., BARRELL B.G.;  
 RL NATURE 310:207-211(1984).  
 CC -1- FUNCTION: PRESUMED VIRION PROTEIN; POSSIBLE ROLE IN DNA  
 PACKAGING (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL6,  
EHV-1 56, EBV BBRFL, HCMV UL104, AND VAV 54.  
CC EMBL: V01555; G59125; -  
DR PIR: A03775; Q08E33.  
DR PIR: S33025; S33025.  
KW LATE PROTEIN.  
SQ SEQUENCE 613 AA; 68456 MW; 69A44AEB CRC32;

Query Match  
Best Local Similarity 82.4%; Score 56; DB 1; Length 613;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 221 SDEYVAY 228  
100 SEDFVAY 107

RESULT 6  
ID KV3C\_HUMAN STANDARD; PRT: 107 AA.  
AC P01596;  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DE IG KAPPA CHAIN V-I REGION (CAR).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
CC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RA MEDLINE: 75075135.  
RX MILSTEIN C.P., DEVESON E.V.;  
RL EUR. J. BIOCHEM. 49:377-391(1974).  
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
DR PIR: A01864; K1H0AR.  
DR HSSP: P01607; IDFB.  
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.  
FT CARBOHYD 28  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11703 MW; 04BF9EED CRC32;

Query Match  
Best Local Similarity 80.9%; Score 55; DB 1; Length 107;  
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 79 ZPBBFAYY 87  
99 ESEDFVAY 107

RESULT 7  
ID KV3C\_HUMAN STANDARD; PRT: 100 AA.  
AC P01621;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN PRECURSOR V-III REGION (NG9) (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
CC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 84093600.  
RA BENTLEY D.L.;  
RL NATURE 307:77-80(1984).  
CC -1- THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.  
DR PIR: A01894; K3HUNG.  
DR HSSP: P01607; IAAG.  
KW IMMUNOGLOBULIN V REGION; SIGNAL; HYBRIDOMA.  
FT NON\_TER 1 1  
FT SIGNAL <1 4  
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION (NG9).  
FT DISULFID 27 93 BY SIMILARITY.

FT NON\_TER 100 100  
SQ SEQUENCE 100 AA; 10729 MW; 99A75223 CRC32;

Query Match  
Best Local Similarity 79.4%; Score 54; DB 1; Length 100;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 84 EPEDFVAY 92  
99 ESEDFVAY 107

RESULT 8  
ID KV3F\_HUMAN STANDARD; PRT: 108 AA.  
AC P01619;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (B6).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
CC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RA MILSTEIN C.P.;  
RL FEBS LETT. 2:301-304(1969).  
CC -1- THIS IS A BENCE-JONES PROTEIN.  
DR PIR: A01891; K3H0B5.  
DR HSSP: P01607; IMCP.  
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.  
FT DISULFID 23 89  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11635 MW; 46D6B68E CRC32;

Query Match  
Best Local Similarity 79.4%; Score 54; DB 1; Length 108;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 80 ZPDEFAYY 88  
99 ESEDFVAY 107

RESULT 9  
ID KV3F\_HUMAN STANDARD; PRT: 109 AA.  
AC P01624;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (POM).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
CC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RA KLAPPER D.G., CAPRA J.D.;  
RL ANN. INST. PASTEUR IMMUNOL. 127C:261-271(1976).  
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.  
DR PIR: A01897; K3H0PM.  
DR HSSP: P01607; IDFB.  
KW IMMUNOGLOBULIN V REGION.  
FT DISULFID 23 89  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA; 11922 MW; A0C42C88 CRC32;

Query Match  
Best Local Similarity 79.4%; Score 54; DB 1; Length 109;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 80 QSEDFVAY 88  
99 ESEDFVAY 107

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DE 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DT IG KAPPA CHAIN V-II REGION (GOL) (RHEUMATOID FACTOR).
OS OSOMO SAPIENS (HUMAN).
OC EUKARYOTA; NEURZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA,
OC EUTHERIA; PRIMATES.
RN (1)
RP SEQUENCE.
RX MEDLINE; 86230578.
RA NEWKIRK M., CHEN P.P., CARSON D.A., POSNETT D., CAPRA J.D.;
RL MOL. IMMUNOL. 23:239-244(1986).
DR PIR: A01893; K3HUGO.
DR HSSP; P01607; IDFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11830 MW; 893DCC4A CRC32;
SQ
Query Match 79.4%; Score 54; DB 1; Length 109;
Best Local Similarity 66.7%; Pred. No. 4.01e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0;
Dd 80 EPEDFAVY 88
1:111 11
Oy 99 ESEDEVAVY 107

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Query Match      79.4%;      Score 54; DB 1; Length 109;
Best Local Similarity 66.7%;      Pred. NO. 4.01e+00;
Matches      6; Conservative      1; Mismatches 2; Indels 0; Gaps 0;

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```

Query Match      79.4%;      Score 54; DB 1; Length 109;
Best Local Similarity 66.7%;      Pred. NO. 4.01e+00;
Matches      6; Conservative      1; Mismatches 2; Indels 0; Gaps 0;

```

```

Query Match      79.4%;      Score 54; DB 1; Length 109;
Best Local Similarity 66.7%;      Pred. NO. 4.01e+00;
Matches      6; Conservative      1; Mismatches 2; Indels 0; Gaps 0;

```

```

Query Match      79.4%;      Score 54; DB 1; Length 109;
Best Local Similarity 66.7%;      Pred. NO. 4.01e+00;
Matches      6; Conservative      1; Mismatches 2; Indels 0; Gaps 0;

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RL NUCLEIC ACIDS RES. 12:9229-9236(1984)
DR EMBL: X01668; -: NOT_ANNOTATED_CDS.
DR PIR: A01900; K3HTVG.
DR HSSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-II1 REGION (VG).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 37E182FC CRC32;

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Query Match
Best Local Similarity 79.4%; Score 54; DB 1; Length 115;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 99 EPEDFAVY 107
Oy 99 ESEDFAVY 107

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RESULT 15
ID KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (REL. 06; CREATED)
DT 01-JAN-1988 (REL. 06; LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16; LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-II1 REGION (IARC/BL41).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86041852.
RA KLOBECK H.G., MEINDL A., COMERIATO G., SOLOMON A., ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
DR EMBL: Z00021; G33179; -
DR PIR: A01899; K3HT41.
DR HSSP: P01607; 3HFM.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-II1 REGION (IARC/BL41).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; 318E08AF CRC32;

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Query Match
Best Local Similarity 79.4%; Score 54; DB 1; Length 128;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 99 EPEDFAVY 107
Oy 99 ESEDFAVY 107

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Search completed: Tue Apr 20 13:59:53 1999  
 Job time : 6 secs.

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RESULT	1	PRELIMINARY;	PRT;	236 AA.
ID	P95945			
AC	P95945;			
DT	01-MAY-1997 (TREMBLREL. 03, CREATED)			
DT	01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)			
DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)			
DE	ENDONUCLEASE III.			
OS	SULFOLOBUS SOLEFATRICUS.			
OC	ARCHAEBACTERIA; CRENARCHAEOTA; SULFOLOBALES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-P2;			
RX	MEDLINE: 97055432.			
RA	SENSE C.W., KIENK H.P., SINGH R.K., ALLARD G., CHAN C.C.Y., LIU Q.Y.,			
RA	PENNY S.L., YOUNG F., SCHEUK M.E., GAASTERLAND T., DOOLITTLE W.F.,			
RA	RAGAN M.A., CHARLEBOIS R.L.;			
RL	EMBL: Y08257; E283822; -. (1996).			
DR	PMOL: Y08257; E283822; -. (1996).			
DR	PRAM: PF00730; Endonuclease_3.			
KM	ENDONUCLEASE.			
SD	SEQUENCE 236 AA: 26843 MW; 31E2C546 CRC32;			
Db	21 EDPIAY 27			
QY	101 EDFVAY 107			
Query Match	82.4%;	Score 56;	DB 1;	Length 236;
Best Local Similarity	85.7%;	Pred. No. 4,586+00;		
Matches	6;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0
RESULT	2	PRELIMINARY;	PRT;	771 AA.
ID	063693			
AC	063693;			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)			
DE	PHODHOLIPASE C DELTA4.			
OS	RATUS NORVIGICUS (RAT).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-DONRYU;			

RX MEDLINE: 96132927.  
RA LIU N., FUKAMI K., YU H., TAKENAWA T.,  
RL J. BIOL. CHEM. 271:355-360(1996).  
DR EMBL: D50455; G1304189; -.  
DR PFAM: PF00036; efnand.  
DR PFAM: PF00168; C2.  
DR PFAM: PF00387; PI-PLC-Y.  
DR PFAM: PF00388; PI-PLC-X.  
SQ SEQUENCE 771 AA; 88862 MW; F347F051 CRC32;

Query Match  
Best Local Similarity 82.4%; Score 56; DB 11; Length 771;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 191 DSEEFVQFY 199  
QY 99 ESEDFVAVY 107

RESULT 3  
AC 062711 PRELIMINARY; PRT; 772 AA.  
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE PHOSPHOLIPASE C DELTA-4.  
OS RATUUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SPRAGUE DAWLEY; TISSUE-BRAIN;  
RX MEDLINE: 96132878.  
RA LEE S.B., RHEE S.G.;  
RL J. BIOL. CHEM. 271:25-31(1996).  
DR EMBL: U1655; G571466; -.  
DR PFAM: PF00168; efnand.  
DR PFAM: PF00387; PI-PLC-Y.  
DR PFAM: PF00388; PI-PLC-X.  
SQ SEQUENCE 772 AA; 88966 MW; 6FE7ACAI CRC32;

Query Match  
Best Local Similarity 82.4%; Score 56; DB 11; Length 772;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

191 DSEEFVQFY 199  
QY 99 ESEDFVAVY 107

RESULT 4  
ID 099818 PRELIMINARY; PRT; 108 AA.  
AC 099818;  
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)  
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE ANTI-SSDNA ANTIBODY LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
GN HUMK3285.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA SUENAGA R.;  
RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U62258; G1773057; -.  
DR PFAM: PF00047; 19.  
FT NON\_TER 1 108  
FT NON\_TER 1 108  
SQ SEQUENCE 108 AA; 11792 MW; 876D5BA3 CRC32;

Query Match  
79.4%; Score 54; DB 4; Length 108;

Best Local Similarity 66.7%; Pred. No. 1.06e+01;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 79 QSEDFVAVY 87  
QY 99 ESEDFVAVY 107

RESULT 5  
ID 014539 PRELIMINARY; PRT; 113 AA.  
AC 014539;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
DE HRV FAB 026-VL (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-PBL.  
RA ITOH K., SUZUKI T.;  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AB006848; D1023046; -.  
DR PFAM: PF00047; 19.  
FT NON\_TER 113  
FT NON\_TER 113  
SQ SEQUENCE 113 AA; 11994 MW; 3CA4456F CRC32;

Query Match  
Best Local Similarity 66.7%; Score 54; DB 4; Length 113;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 81 EPEDFVAVY 89  
QY 99 ESEDFVAVY 107

RESULT 6  
ID 014538 PRELIMINARY; PRT; 114 AA.  
AC 014538;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
DE HRV FAB N28-VL (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-PBL.  
RA ITOH K., SUZUKI T.;  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AB006845; D1023044; -.  
DR PFAM: PF00047; 19.  
FT NON\_TER 114  
FT NON\_TER 114  
SQ SEQUENCE 114 AA; 12283 MW; BE57FD0 CRC32;

Query Match  
Best Local Similarity 79.4%; Score 54; DB 4; Length 114;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 82 EPEDFVAVY 90  
QY 99 ESEDFVAVY 107

RESULT 7  
ID 014537 PRELIMINARY; PRT; 115 AA.  
AC 014537;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
DE HRV FAB N27-VL (FRAGMENT).  
SQ SEQUENCE 115 AA; 12283 MW; BE57FD0 CRC32;



OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PBL;  
 RA ITOH K., SUZUKI T.;  
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; AB006844; D1023043; -.  
 DR PFAM; PF00047; 15.  
 FT NON\_TER 115 115  
 SO SEQUENCE 115 AA; 12417 MW; 96E3C279 CRC32;  
 Query Match 79.4%; Score 54; DB 4; Length 115;  
 Best Local Similarity 66.7%; Pred. No. 1.06e+01;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Db 82 ESEDFVAY 90  
 Y 99 ESEDFVAY 107

RESULT 8  
 ID 042983; PRELIMINARY; PRT; 251 AA.  
 AC 042983;  
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 28.9 KD PROTEIN.  
 GN SPBC349.03C.  
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOTECETES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972H-;  
 RA LYNE M., PURNELLE B., GOFFEAU A., WOOD V., RAJANDREAM M.A.,  
 RL BARRELL B.G.;  
 RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; AL021816; E1250650; -.  
 KW HYPOTHETICAL PROTEIN.  
 SO SEQUENCE 251 AA; 28915 MW; 93F693A6 CRC32;  
 Query Match 79.4%; Score 54; DB 3; Length 251;  
 Best Local Similarity 57.1%; Pred. No. 1.06e+01;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 235 DEFVSYY 241  
 Y 101 EDFVAY 107

RESULT 9  
 ID 013217; PRELIMINARY; PRT; 504 AA.  
 AC 013217;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE PROTEIN KINASE INHIBITOR P58.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 96235132.  
 RA KORTH M.J., LYONS C.N., WAMBACH M., KATZE M.G.;  
 RL GENE 170:181-188(1996).  
 DR EMBL; U28424; G1353270; -.  
 DR PFAM; PF00226; DnaJ.  
 DR PFAM; PF00515; TPR.  
 SO SEQUENCE 504 AA; 57580 MW; 86270C88 CRC32;  
 Query Match 79.4%; Score 54; DB 4; Length 504;  
 Best Local Similarity 33.3%; Pred. No. 1.06e+01;

Db 67 DPNYIAY 75  
 Y 99 ESEDFVAY 107

RESULT 10  
 ID 060873; PRELIMINARY; PRT; 504 AA.  
 AC 060873;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE PROTEIN KINASE, INTERFERON INDUCIBLE DOUBLE STRANDED RNA  
 DE (PROTEIN KINASE INHIBITOR P58).  
 GN PKRI.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 96235132.  
 RA KORTH M.J., LYONS C.N., WAMBACH M., KATZE M.G.;  
 RL GENE 170:181-188(1996).  
 DR EMBL; U28423; G1353272; -.  
 DR MGD; MGI:107373; PRKRI.  
 DR PFAM; PF00226; DnaJ.  
 DR PFAM; PF00515; TPR.  
 SO SEQUENCE 504 AA; 57666 MW; 89862747 CRC32;  
 Query Match 79.4%; Score 54; DB 11; Length 504;  
 Best Local Similarity 33.3%; Pred. No. 1.06e+01;  
 Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 67 DPNYIAY 75  
 Y 99 ESEDFVAY 107

RESULT 11  
 ID 027968; PRELIMINARY; PRT; 504 AA.  
 AC 027968;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE PRK INHIBITOR P58.  
 OS BOS TAURUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; ARTIODACTYLA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 94187704.  
 RA LEE T.G., TANG N., THOMPSON S., MILLER J., KATZE M.G.;  
 RL MOL. CELL. BIOL. 14:2331-2342(1994).  
 DR EMBL; U04631; G468012; -.  
 DR PFAM; PF00226; DnaJ.  
 DR PFAM; PF00515; TPR.  
 KW PROTEIN KINASE.  
 SO SEQUENCE 504 AA; 57704 MW; 0DB8EEB4 CRC32;  
 Query Match 79.4%; Score 54; DB 6; Length 504;  
 Best Local Similarity 33.3%; Pred. No. 1.06e+01;  
 Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 67 DPNYIAY 75  
 Y 99 ESEDFVAY 107

RESULT 12  
 ID 061588; PRELIMINARY; PRT; 81 AA.  
 AC 061588;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 Query Match 79.4%; Score 54; DB 6; Length 504;  
 Best Local Similarity 33.3%; Pred. No. 1.06e+01;  
 Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 GN 08(ANTI-MRBC HYBRIDOMA) LIGHT CHAIN.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 RN EUTHERIA; RODENTIA.  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NZB.  
 RX MEDLINE; 92185208.  
 RA CAULFIELD M.J., STANKO D.;  
 RL J. IMMUNOL. 148:2068-2073(1992).  
 DR EMBL; X60425; E41199;  
 DR PFM; PF00047; 19.  
 SQ SEQUENCE 81 AA; 8945 MM; 5AF33092 CRC32;

Query Match  
 Best Local Similarity 66.7%; Score 53; DB 11; Length 81;  
 Pred. No. 1.60e+01;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 56 QSDDFAVY 64  
 QY 99 ESEDFVAY 107

RESULT 13  
 ID 016078 PRELIMINARY; PRT; 93 AA.  
 AC 016078;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE RF-V KAPPA 1-RHEUMATOID FACTOR V KAPPA REGION (CLONE SLK7)  
 DE (FRAGMENT).  
 GN RF-V<KAPPA>1.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 RN EUTHERIA; PRIMATES.  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 94033036.  
 RA MARTIN T., CROUZIER R., BLAISON G., LEVALLLOIS H., PASQUALI J.L.;  
 RL AUTOIMMUNITY 15:163-170(1993).  
 DR EMBL; S67060; E98154;  
 DR PFM; PF00047; 19.  
 FT NON\_TER 1  
 FT NON\_TER 93  
 SEQUENCE 93 AA; 10178 MM; 610E33C1 CRC32;

Query Match  
 Best Local Similarity 55.6%; Score 53; DB 4; Length 93;  
 Pred. No. 1.60e+01;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 64 QSDDFAVY 72  
 QY 99 ESEDFVAY 107

RESULT 14  
 ID 016079 PRELIMINARY; PRT; 94 AA.  
 AC 016079;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE RF-V KAPPA 1-RHEUMATOID FACTOR V KAPPA REGION (CLONE BKV42)  
 DE (FRAGMENT).  
 GN RF-V<KAPPA>1.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 RN EUTHERIA; PRIMATES.  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 94033036.

RA MARTIN T., CROUZIER R., BLAISON G., LEVALLLOIS H., PASQUALI J.L.;  
 RL AUTOIMMUNITY 15:163-170(1993).  
 DR EMBL; S67061; E98155;  
 DR PFM; PF00047; 19.  
 FT NON\_TER 1  
 FT NON\_TER 94  
 SEQUENCE 94 AA; 10360 MM; 746D2A79 CRC32;

Query Match  
 Best Local Similarity 55.6%; Score 53; DB 4; Length 94;  
 Pred. No. 1.60e+01;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 64 QSDDFAVY 72  
 QY 99 ESEDFVAY 107

RESULT 15  
 ID 099514 PRELIMINARY; PRT; 105 AA.  
 AC 099514;  
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)  
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)  
 DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DE LIGHT CHAIN FAB FRAGMENT (FRAGMENT).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 RN EUTHERIA; PRIMATES.  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RA HORN M.P., VOGEL M., BIAGI C., MIESCHER S.M., STADLER B.M.;  
 RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; Y08148; E274854;  
 DR PFM; PF00047; 19.  
 FT NON\_TER 1  
 FT NON\_TER 105  
 SEQUENCE 105 AA; 11303 MM; 249B7EC3 CRC32;

Query Match  
 Best Local Similarity 55.6%; Score 53; DB 4; Length 105;  
 Pred. No. 1.60e+01;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 77 QSDDFAVY 85  
 QY 99 ESEDFVAY 107

Search completed: Tue Apr 20 14:00:47 1999  
 Job time : 37 secs.

\*\*\*\*\*  
M P E S E E H  
(TM)  
\*\*\*\*\*

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Mpsrch.p protein - protein database search, using Smith-Waterman algorithm  
on: Tue Apr 20 14:08:23 1999; Maspar time 2.95 Seconds  
tabular output not generated. ---114.088 Million cell updates/sec

Title: >US-08-836-455-1\_1  
Description: (89-97) from trans.pep (3 of 3)  
Perfect Score: 54  
Sequence: 1 SDYSLTSS 9

Scoring table: PAM 150  
Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: P1r58  
1:plrl 2:plrl2 3:plrl3 4:plrl4

Statistics: Mean 22.382; Variance 27.684; scale 0.808

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

sult	Query	Match	Length	DB	ID	Description	Pred. No.
No.	Score						
1	54	100.0	88	2	PL0261	Ig kappa chain V regi	4.80e-01
2	54	100.0	91	2	SI1622	Ig kappa chain V regi	4.80e-01
3	54	100.0	98	2	PH1062	Ig light chain V regi	4.80e-01
4	54	100.0	106	2	PL0260	Ig kappa chain V regi	4.80e-01
5	54	100.0	106	2	PL0259	Ig kappa chain V regi	4.80e-01
6	54	100.0	106	2	PL0262	Ig kappa chain V regi	4.80e-01
7	54	100.0	108	4	B47271	nitrophenyl phosphon	4.80e-01
8	54	100.0	129	4	B23986	Ig kappa chain precu	4.80e-01
9	54	100.0	129	2	D32513	Ig kappa chain precu	4.80e-01
10	54	100.0	130	1	KYMSM4	Ig kappa chain precu	4.80e-01
11	50	92.6	75	2	A34966	Ig heavy chain V regi	3.42e+00
12	50	92.6	98	2	PH1065	Ig kappa chain V regi	3.42e+00
13	50	92.6	101	2	SI3701	Ig kappa chain V regi	3.42e+00
14	50	92.6	101	2	C28840	Ig kappa chain V regi	3.42e+00
15	50	92.6	101	2	B28840	Ig kappa chain V regi	3.42e+00
16	50	92.6	103	2	SI3703	Ig kappa chain V regi	3.42e+00
17	50	92.6	104	2	SI3700	Ig kappa chain V regi	3.42e+00
18	50	92.6	115	1	KYMSM6	Ig kappa chain precu	3.42e+00
19	50	92.6	117	2	SI1668	Ig kappa chain V regi	3.42e+00
20	50	92.6	117	2	SI1814	Ig kappa chain V regi	3.42e+00
21	50	92.6	120	2	SI1666	Ig kappa chain V regi	3.42e+00
22	50	92.6	120	2	SI1667	Ig kappa chain V regi	3.42e+00
23	50	92.6	127	2	SS2447	Ig kappa chain V regi	3.42e+00

24	50	92.6	152	2	S30751	Ig kappa chain precu	3.42e+00
25	50	92.6	234	2	SI4237	Ig kappa chain precu	3.42e+00
26	49	90.7	105	2	PH0087	Ig kappa chain V regi	5.51e+00
27	49	90.7	107	2	B28044	Ig kappa chain V regi	5.51e+00
28	49	90.7	107	2	S69901	Ig kappa chain (clone	5.51e+00
29	49	90.7	107	2	S32188	Ig kappa chain V regi	5.51e+00
30	49	90.7	107	2	B49026	Ig kappa chain V regi	5.51e+00
31	49	90.7	108	2	SI1124	Ig kappa chain V regi	5.51e+00
32	49	90.7	108	2	C26405	Ig kappa chain V regi	5.51e+00
33	49	90.7	108	2	B26405	Ig kappa chain V regi	5.51e+00
34	49	90.7	108	2	B30551	Ig kappa chain V regi	5.51e+00
35	49	90.7	108	2	S69902	Ig kappa chain (clone	5.51e+00
36	49	90.7	108	2	S69903	Ig kappa chain V regi	5.51e+00
37	49	90.7	108	2	S38862	Ig kappa chain V regi	5.51e+00
38	49	90.7	109	2	PH0888	Ig kappa chain V regi	5.51e+00
39	49	90.7	111	2	A58740	Ig kappa chain V regi	5.51e+00
40	49	90.7	111	2	C38740	Ig kappa chain V regi	5.51e+00
41	49	90.7	115	2	A53276	Ig kappa chain V regi	5.51e+00
42	49	90.7	115	2	JI0080	Ig kappa chain precu	5.51e+00
43	49	90.7	122	2	A29380	Ig kappa chain precu	5.51e+00
44	49	90.7	128	2	PL0101	Ig kappa chain precu	5.51e+00
45	49	90.7	128	2	A26406	Ig kappa chain V regi	5.51e+00

## ALIGNMENTS

RESULT	1	ALIGNMENTS
ENTRY	PL0261	#type fragment
TITLE	Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)	
ORGANISM	#formal_name Mus musculus #common_name house mouse	
DATE	16-Sep-1992 #sequence_rev15on 16-Sep-1992 #text_change 09-May-1997	
ACCESSIONS	PL0261	
REFERENCE	PL0231	
#authors	Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Weigert, M.	
#journal	J. Exp. Med. (1990) 171:265-297	
#title	Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.	
#cross-references	W01D:90111618	
#accession	PL0261	
#molecule_type	mRNA	
CLASSIFICATION	#residues 1-88 #label SHL	
KEYWORDS	#superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin	
FEATURE	1-5	
1-5	#region framework 1\	
6-16	#region complementarity-determining 1\	
17-31	#region framework 2\	
32-38	#region complementarity-determining 2\	
39-70	#region framework 3\	
71-79	#region complementarity-determining 3\	
80-88	#region framework 4	
SUMMARY	#length 88 #checksum 7092	
Query Match	100.0%; Score 54; DB 2; Length 88;	
Best Local Similarity	100.0%; Pred. No. 4.80e-01;	
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	51 SDYSLTSS 59	
QY	89 SDYSLTSS 97	
RESULT	2	
ENTRY	SI1622	#type complete
TITLE	Ig kappa chain V region - mouse	
ORGANISM	#formal_name Mus musculus #common_name house mouse	
DATE	22-Nov-1993 #sequence_rev15on 10-Nov-1995 #text_change 09-May-1997	
ACCESSIONS	SI1622	
REFERENCE	SI1730	
#authors	Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.	

```

#Journal      Nature (1991) 352:624-628
#title        Making antibody fragments using phage display libraries.
#cross-references MUID:91326098
#accession    S17622
#status       preliminary
#molecule_type nucleic acid
#residues     1-91 #label CIA
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        length 91 #molecular_weight 9895 #checksum 3446

Query Match      100.0%; Score 54; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 4.80e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 SDYSTITSS 69
QY 89 SDYSTITSS 97

RESULT 3
ENTRY      PH1062      #type fragment
TITLE      Ig light chain V region (clone 202.105) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
          15-Jun-1996
ACCESSIONS PH1062
REFERENCE   PH1062
#authors    Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
#journal    J. Exp. Med. (1992) 176:761-779
#title      Both IgM and IgG anti-DNA antibodies are the products of
            clonally selective B cell stimulation in (NZB x NZW)F1
            mice.
#accession  PH1062
#status     nucleic acid sequence not shown
#molecule_type mRNA
#residues   1-98 #label TIL
#KEYWORDS   #experimental_source B cell, strain (NZB x NZW)F1
            #superfamily immunoglobulin V region; immunoglobulin homology
            #immunoglobulin
SUMMARY      length 98 #checksum 6933

Query Match      100.0%; Score 54; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.80e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

69 SDYSTITSS 77
QY 89 SDYSTITSS 97

RESULT 4
ENTRY      PL0260      #type fragment
TITLE      Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
          16-Aug-1996
ACCESSIONS PL0260
REFERENCE   PL0260
#authors    Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
            D.; Marshak-Rothstein, A.; Weigert, M.
#journal    J. Exp. Med. (1990) 171:265-297
#title      Anti-DNA antibodies from autoimmune mice arise by clonal
            expansion and somatic mutation.
#cross-references MUID:90111618
#accession  PL0260
#molecule_type mRNA
#residues   1-106 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        1-23
            #region framework 1\
            #region complementarity-determining 1\
            #region framework 2\
            #region complementarity-determining 2\
            #region framework 3\
            #region complementarity-determining 3\
            #region framework 4
SUMMARY      length 106 #checksum 2162

Query Match      100.0%; Score 54; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.80e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

69 SDYSTITSS 77
QY 89 SDYSTITSS 97

RESULT 5
ENTRY      PL0259      #type fragment
TITLE      Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
          16-Aug-1996
ACCESSIONS PL0259
REFERENCE   PL0259
#authors    Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
            D.; Marshak-Rothstein, A.; Weigert, M.
#journal    J. Exp. Med. (1990) 171:265-297
#title      Anti-DNA antibodies from autoimmune mice arise by clonal
            expansion and somatic mutation.
#cross-references MUID:90111618
#accession  PL0259
#molecule_type mRNA
#residues   1-106 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        1-23
            #region framework 1\
            #region complementarity-determining 1\
            #region framework 2\
            #region complementarity-determining 2\
            #region framework 3\
            #region complementarity-determining 3\
            #region framework 4
SUMMARY      length 106 #checksum 2162

Query Match      100.0%; Score 54; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.80e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

69 SDYSTITSS 77
QY 89 SDYSTITSS 97

RESULT 6
ENTRY      PL0262      #type fragment
TITLE      Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
          16-Aug-1996
ACCESSIONS PL0262
REFERENCE   PL0262
#authors    Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
            D.; Marshak-Rothstein, A.; Weigert, M.
#journal    J. Exp. Med. (1990) 171:265-297
#title      Anti-DNA antibodies from autoimmune mice arise by clonal
            expansion and somatic mutation.
#cross-references MUID:90111618
#accession  PL0262
#molecule_type mRNA
#residues   1-106 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        1-23
            #region framework 1\
            #region complementarity-determining 1\

```

FEATURE 1-23 #region framework 1\  
24-34 #region complementarity-determining 1\  
35-49 #region complementarity-determining 2\  
50-56 #region complementarity-determining 3\  
57-88 #region framework 3\  
89-97 #region complementarity-determining 4\  
98-106 #region framework 4  
SUMMARY #length 106 #checksum 658

Query Match 100.0%; Score 54; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 4.80e-01;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 69 SDYSLTSS 77  
OY 89 SDYSLTSS 97

SULT 7  
ENTRY B47271 #type fragment  
TITLE nitrophenyl phosphate-specific antibody 48G7 light chain V  
ORGANISM #formal\_name synthetic  
#note Mus musculus (house mouse) gene engineered and expressed in Escherichia coli  
DATE 21-Sep-1993 #sequence\_revision 11-Aug-1995 #text\_change 11-Aug-1995

ACCESSIONS B47271  
REFERENCE A47271  
#authors Lesley, S.A.; Pattem, P.A.; Schultz, P.G.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1160-1165  
#title A genetic approach to the generation of antibodies with enhanced catalytic activities.  
#cross-references MUID:9316560  
#accession B47271  
#molecule\_type DNA; protein  
#residues 1-108 #label IES  
#note sequence extracted from NCBI backbone (NCBIN:124856, NCBIPI:124859)  
##note parts of this sequence were determined by protein sequencing  
#note

FEATURE 24-89  
SUMMARY #disulfide\_bonds #status predicted  
#length 108 #checksum 9036

Query Match 100.0%; Score 54; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 4.80e-01;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 SDYSLTSS 78  
OY 89 SDYSLTSS 97

RESULT 8  
ENTRY B23986 #type complete  
TITLE Ig kappa chain precursor V region (IR2) - rat  
ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 17-Sep-1987 #sequence\_revision 17-Sep-1987 #text\_change 16-Aug-1996

ACCESSIONS B23986  
REFERENCE A91541  
#authors Hellman, L.; Engstrom, A.; Bennich, H.; Petersson, U.  
#journal Gene (1985) 40:107-114  
#title Structure and expression of kappa-chain genes in two IGE-producing rat immunocytomas.  
#cross-references MUID:86137406  
#accession B23986  
#molecule\_type mRNA  
#residues 1-129 #label HEL  
#journal heterotetramer; immunoglobulin

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS

SUMMARY #length 129 #molecular\_weight 14217 #checksum 5336

Query Match 100.0%; Score 54; DB 2; Length 129;  
Best Local Similarity 100.0%; Pred. No. 4.80e-01;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 SDYSLTSS 99  
OY 89 SDYSLTSS 97

RESULT 9  
ENTRY D32513 #type complete  
TITLE Ig kappa chain precursor V region (BXW16) - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 20-Mar-1998

ACCESSIONS D32513  
REFERENCE A94689  
#authors Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos, A.N.  
#journal J. Clin. Invest. (1988) 82:852-860  
#title Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice.  
#cross-references MUID:88331394  
#accession D32513  
#molecule\_type DNA  
#residues 1-129 #label KOF  
#cross-references GB:M20832; NID:9196941; PID:9196942  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SUMMARY #length 129 #molecular\_weight 14097 #checksum 3457

Query Match 100.0%; Score 54; DB 2; Length 129;  
Best Local Similarity 100.0%; Pred. No. 4.80e-01;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 SDYSLTSS 99  
OY 89 SDYSLTSS 97

RESULT 10  
ENTRY KVMSM4 #type complete  
TITLE Ig kappa chain precursor V region (MOPC 41) - mouse  
CONTAINS Ig kappa chain precursor V region VK41  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 16-Aug-1996

ACCESSIONS A93211; B93211; A93815; A94239; A01922; A01923  
REFERENCE A93211  
#authors Seidman, J.G.; Max, E.E.; Leder, P.  
#journal Nature (1979) 280:370-375  
#title A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.  
#cross-references MUID:79221900  
#accession A93211  
#molecule\_type DNA  
#residues 1-130 #label PC41  
#accession B93211  
#molecule\_type DNA  
#residues 1-117 #label VK41  
#note the sequences were determined from the differentiated gene MOPC 41 and the germline gene VK41

REFERENCE A93815  
#authors Burslein, Y.; Schechter, I.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720  
#title Amino acid sequence of the NH-2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda-1-type and kappa-type light chains.  
#cross-references MUID:77148916

```

#accession      A93815          --
#molecule_type protein
##residues      1-33 ##label BUR
#note            Met-3 is apparently used as an alternative initiator in
                  25% of the chains

REFERENCE
#authors         A94239
#journal         Gray, W.R.; Dreyer, W.J.; Hood, L.
#title           Science (1967) 155:465-467
                  Mechanism of antibody synthesis: size differences between
                  mouse kappa chains.
#cross-references #molecule-type protein
#accession       A94239
##residues      23-49,'B','51-53','LSB','57-58','ZZ','61-62','BZ','65-76','B',
                  78-108,110-130 ##label GRA
#experimental_source Bence Jones protein MOPC 41

GENETICS
#introns
#PLEX            19/1
                  An immunoglobulin heterotetramer subunit consists of two
                  identical light (kappa or lambda) and two identical heavy
                  (alpha, delta, epsilon, gamma, or mu) chains usually
                  stabilized by interchain disulfide bonds. In some cases,
                  such as IgA and IgM, the subunits associate into larger
                  oligomers.
CLASSIFICATION
KEYWORDS         #superfamily immunoglobulin V region; immunoglobulin homology
FEATURES         #alternative initiators; heterotetramer; immunoglobulin
                  1-22
                  #domain signal sequence #status experimental #label
                  SigI\
                  #intra signal sequence #status experimental #label
                  Sig2\
                23-130 #product Ig kappa chain V region (MOPC 41) #status
                    experimental #label M41\
                    #domain immunoglobulin homology #label IM\
                    #disulfide_bonds #status predicted
SUMMARY          #length 130 #molecular_weight 14311 #checksum 6707

Query Match
Best Local Similarity 100.0%; Pred. No. 4,80e-01; Length 130;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db    91 SDYSLTSS 99
      |||||||
Qy    89 SDYSLTSS 97

MULT 11
NAME
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references #molecule-type protein
#accession       A34966
##residues      23-49,'B','51-53','LSB','57-58','ZZ','61-62','BZ','65-76','B',
                  78-108,110-130 ##label GRA
#experimental_source Bence Jones protein MOPC 41

GENETICS
#introns
#PLEX            19/1
                  An immunoglobulin heterotetramer subunit consists of two
                  identical light (kappa or lambda) and two identical heavy
                  (alpha, delta, epsilon, gamma, or mu) chains usually
                  stabilized by interchain disulfide bonds. In some cases,
                  such as IgA and IgM, the subunits associate into larger
                  oligomers.
CLASSIFICATION
KEYWORDS         #superfamily immunoglobulin V region; immunoglobulin homology
FEATURES         #alternative initiators; heterotetramer; immunoglobulin
                  1-22
                  #domain signal sequence #status experimental #label
                  SigI\
                  #intra signal sequence #status experimental #label
                  Sig2\
                23-130 #product Ig kappa chain V region (MOPC 41) #status
                    experimental #label M41\
                    #domain immunoglobulin homology #label IM\
                    #disulfide_bonds #status predicted
SUMMARY          #length 130 #molecular_weight 14311 #checksum 6707

Query Match
Best Local Similarity 100.0%; Pred. No. 4,80e-01; Length 130;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db    91 SDYSLTSS 99
      |||||||
Qy    89 SDYSLTSS 97

MULT 11
NAME
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references #molecule-type protein
#accession       A34966
##residues      23-49,'B','51-53','LSB','57-58','ZZ','61-62','BZ','65-76','B',
                  78-108,110-130 ##label GRA
#experimental_source Bence Jones protein MOPC 41

GENETICS
#introns
#PLEX            19/1
                  An immunoglobulin heterotetramer subunit consists of two
                  identical light (kappa or lambda) and two identical heavy
                  (alpha, delta, epsilon, gamma, or mu) chains usually
                  stabilized by interchain disulfide bonds. In some cases,
                  such as IgA and IgM, the subunits associate into larger
                  oligomers.
CLASSIFICATION
KEYWORDS         #superfamily immunoglobulin V region; immunoglobulin homology
FEATURES         #alternative initiators; heterotetramer; immunoglobulin
                  1-22
                  #domain signal sequence #status experimental #label
                  SigI\
                  #intra signal sequence #status experimental #label
                  Sig2\
                23-130 #product Ig kappa chain V region (MOPC 41) #status
                    experimental #label M41\
                    #domain immunoglobulin homology #label IM\
                    #disulfide_bonds #status predicted
SUMMARY          #length 130 #molecular_weight 14311 #checksum 6707

Query Match
Best Local Similarity 100.0%; Pred. No. 3,42e+00; Length 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db      41 DYSTLISS 48
|||||||
Qy      90 DYSTLISS 97

RESULT 12
ENTRY   PH1065 #type fragment
TITLE   Ig kappa chain V region (clone 163.47) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
13-Feb-1998

ACCESSIONS
REFERENCE PH1065
#authors TILLMAN, D.M.; YU, N.T.; HILL, R.J.; MARION, T.N.
#journal J. Exp. Med. (1992) 176:761-779
#title Both IgM and IgG anti-DNA antibodies are the products of
clonally selective B cell stimulation in (NZB x NZM)F1
mice.

#accession PH1065
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-98 #label til
#experimental_source B cell, strain [NZB x NZM]F1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
SUMMARY #length 98 #checksum 4553

Query Match 92.6%; Score 50; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.42e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      70 DYSTLISS 77
|||||||
Qy      90 DYSTLISS 97

RESULT 13
ENTRY   S13701 #type fragment
TITLE   Ig kappa chain V region (hybridoma NC19-E11) - mouse
         (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     21-Nov-1993 #sequence_revision 10-Nov-1993 #text_change
09-May-1997

ACCESSIONS
REFERENCE S13701
#authors PENNELL, C.A.; MERCOLINO, T.J.; GRIFONE, T.A.; ARNOLD, L.W.;
HAUGHTON, G.; CLARKE, S.H.
#journal Eur. J. Immunol. (1989) 19:1289-1295
#title B cells due to clonal selection.
#cross-references MVID:89338557
#accession S13701
#status preliminary
#molecule_type mRNA
#residues 1-101 #label PEN
#cross-references EMBL:X53354
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 101 #checksum 6598

Query Match 92.6%; Score 50; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.42e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      70 DYSTLISS 77
|||||||
Qy      90 DYSTLISS 97

RESULT 14
ENTRY   C28840 #type fragment
TITLE   Ig kappa chain V region (HP22) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse

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DATE 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change

ACCESSIONS 16-Aug-1996

C28840; J25114

REFERENCE

#authors

Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.

#journal

EMBO J. (1985) 4:3681-3688

#title

The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.

#cross-references MUID:86136012

#accession

C28840

#molecule\_type mRNA

#residues 1-101 #label OIL

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS heterotetramer; immunoglobulin

SUMMARY #length 101 #checksum 5983

Query Match

Best Local Similarity 100.0%; Score 50; DB 2; Length 101;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 64 DYSLRSS 71

QY 90 DYSLRSS 97

RESULT 15

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#accession

#molecule\_type mRNA

#residues

CLASSIFICATION

KEYWORDS

SUMMARY

Query Match

Best Local Similarity 100.0%; Score 50; DB 2; Length 101;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 64 DYSLRSS 71

QY 90 DYSLRSS 97

Search completed: Tue Apr 20 14:08:41 1999

Job time : 18 secs.

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 SDYSLTSS 99  
| | | | | | | |  
QY 89 SDYSLTSS 97

RESULT 2  
ID KVSF\_MOUSE STANDARD; PRT; 115 AA.  
AC P01638:

DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN PRECURSOR V-V REGION (L6) (FRAGMENT).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
[1]

SEQUENCE FROM N.A.  
MEDLINE; 81220975.  
PECH M., HOCHTL J., SCHNELL H., ZACHAU H.G.;

RL NATURE 291:668-670(1981).  
PIR: A01921; KVM5L6.  
DR HSSP: P01607; IIF.

KW IMMUNOGLOBULIN V REGION; SIGNAL.  
FT SIGNAL 1 20

FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION (L6).  
FT DOMAIN 21 43 FRAMEWORK-1.

FT DOMAIN 44 34 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 55 69 FRAMEWORK 2.

FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 77 108 FRAMEWORK 3.

FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING 3.  
FT DISULFID 43 108 BY SIMILARITY.  
FT NON\_TER 115 115

SO SEQUENCE 115 AA; 12986 MW; 958689AF CRC32;  
Query Match 92.6%; Score 50; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 4.56e-01;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 DYSLTSS 97  
| | | | | | | |  
QY 90 DYSLTSS 97

LT 3  
KVSK\_MOUSE STANDARD; PRT; 108 AA.  
P01644:

DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-V REGION (HP R16.7).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
[1]

SEQUENCE.  
RC STRAIN-A/J;  
RX MEDLINE; 82150934.

RA SIEGELMAN M., CAPRA J.D.;  
PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).

CC -1- ANTI-ARSONATE HYBRIDOMA PROTEIN.  
PIR: A01927; KVM5AR.

DR HSSP: P01607; IFAI.  
KW IMMUNOGLOBULIN V REGION; ANTARSONATE ANTIBODY.  
FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 35 49 FRAMEWORK 2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 57 88 FRAMEWORK 3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 98 108 FRAMEWORK 4.

FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SO SEQUENCE 108 AA; 11910 MW; 64A62905 CRC32;

Query Match 90.7%; Score 49; DB 1; Length 108;  
Best Local Similarity 77.8%; Pred. No. 8.08e-01;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 69 TDYSLTSS 77  
: | | | | | | | |  
QY 89 SDYSLTSS 97

RESULT 4  
ID KVSJ\_MOUSE STANDARD; PRT; 108 AA.  
AC P01643:

DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-V REGION (MOPC 173).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
[1]

SEQUENCE.  
RX MEDLINE; 76091934.  
RA SCHIFF C., RODGERAU M.;

RL EUR. J. BIOCHEM. 59:525-537(1975).  
PIR: A01926; KVM573.

DR HSSP: P01607; IFAI.  
KW IMMUNOGLOBULIN V REGION.

FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 35 49 FRAMEWORK 2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 57 88 FRAMEWORK 3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 98 108 FRAMEWORK 4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108

SO SEQUENCE 108 AA; 11819 MW; EA186054 CRC32;  
Query Match 90.7%; Score 49; DB 1; Length 108;  
Best Local Similarity 77.8%; Pred. No. 8.08e-01;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 69 TDYSLTSS 77  
: | | | | | | | |  
QY 89 SDYSLTSS 97

RESULT 5  
ID KVSJ\_MOUSE STANDARD; PRT; 108 AA.  
AC P01647:

DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-V REGION (HP 144E1).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
[1]

SEQUENCE.  
RC STRAIN-A/J;  
RX MEDLINE; 82150934.

RA SIEGELMAN M., CAPRA J.D.;  
PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).

CC -1- ANTI-ARSONATE HYBRIDOMA PROTEIN.  
PIR: A01927; KVM5AR.

DR HSSP: P01607; IFAI.  
KW IMMUNOGLOBULIN V REGION; ANTARSONATE ANTIBODY.  
FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 108 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11965 MM; 84754175 CRC32;

Query Match  
 Best Local Similarity 77.8%; Score 49; DB 1; Length 108;  
 Pred. No. 8.08e-01;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 69 TDYSLTISN 77  
 QY 89 SDYSLTIS 97

ULT 6 STANDARD; PRT: 108 AA.  
 P01648; KVSQ\_MOUSE

DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-V REGION (HP 91A3).  
 OS MUS MUSCULUS (MOUSE).  
 OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.

RP SEQUENCE.  
 RX STRAIN-A/J;  
 RX MEDLINE: 82150934.  
 RA STEGELMAN M., CAPRA J.D.;  
 RA PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).  
 CC -1- ANTI-ARSONATE HYBRIDOMA PROTEIN.  
 DR HSP: A01927; KVSAR.  
 DR HSP: P01607; IPAT.  
 KM IMMUNOGLOBULIN V REGION; ANTARSONATE ANTIBODY.

FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 108 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11961 MM; 58067780 CRC32;

Query Match  
 Best Local Similarity 77.8%; Score 49; DB 1; Length 108;  
 Pred. No. 8.08e-01;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 69 TDYSLTISN 77  
 QY 89 SDYSLTIS 97

RESULT 7 STANDARD; PRT: 108 AA.  
 AC P01645; KVSQ\_MOUSE

DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-V REGION (HP 9367).  
 OS MUS MUSCULUS (MOUSE).  
 OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RP SEQUENCE.  
 RX STRAIN-A/J;  
 RX MEDLINE: 82150934.

RA SIEGELMAN M., CAPRA J.D.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).  
 CC -1- ANTI-ARSONATE HYBRIDOMA PROTEIN.  
 DR PIR: A01927; KVSAR.  
 DR HSP: P01607; IPAT.

KM IMMUNOGLOBULIN V REGION; ANTARSONATE ANTIBODY.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 108 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11954 MM; A203E130 CRC32;

Query Match  
 Best Local Similarity 77.8%; Score 49; DB 1; Length 108;  
 Pred. No. 8.08e-01;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 69 TDYSLTISN 77  
 QY 89 SDYSLTIS 97

RESULT 8 STANDARD; PRT: 108 AA.  
 ID KVSQ\_MOUSE

AC P01646;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-V REGION (HP 123E6).  
 OS MUS MUSCULUS (MOUSE).  
 OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.

RP SEQUENCE.  
 RX STRAIN-A/J;  
 RX MEDLINE: 82150934.  
 RA SIEGELMAN M., CAPRA J.D.;  
 RA PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).  
 CC -1- ANTI-ARSONATE HYBRIDOMA PROTEIN.  
 DR PIR: A01927; KVSAR.  
 DR HSP: P01607; IPAT.

KM IMMUNOGLOBULIN V REGION; ANTARSONATE ANTIBODY.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 108 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11989 MM; 23B8B67 CRC32;

Query Match  
 Best Local Similarity 77.8%; Score 49; DB 1; Length 108;  
 Pred. No. 8.08e-01;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 69 TDYSLTISN 77  
 QY 89 SDYSLTIS 97

RESULT 9 STANDARD; PRT: 108 AA.  
 ID KVSQ\_MOUSE

AC P04946;  
 DT 13-AUG-1987 (REL. 05, CREATED)  
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-V REGION (N05-89.4).

OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE: 83271467.  
 RA KAARINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;  
 RL NATURE 304:320-324 (1983).  
 CC -1- ANTI-2-PHENYL OXAZOLONE (PROX) ANTIBODY.  
 DR EMBL: K00745; G196455; -.  
 DR HSS: P01607; 1F41.  
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 107 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11866 MW; D396F142 CRC32;  
 Query Match 87.0%; Score 47; DB 1; Length 108;  
 Best Local Similarity 66.7%; Pred. No. 2.47e+00;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Db 69 TDSLTSTN 77  
 QY 89 SDYSLTSS 97  
 RESULT 10  
 ID Y113.CABEL STANDARD; PRT; 435 AA.  
 AC Q10917;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 48.6 KD PROTEIN B0252.3 IN CHROMOSOME II.  
 GN B0252.3  
 OS CAENORHABDITIS ELEGANS.  
 OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 PA DU 2, WATERSTON R.;  
 SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 EMBL: U23453; G733576; -.  
 DR WORMPEP: B0252.3; CE02419.  
 KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE.  
 FT TRANSMEM 55 75 POTENTIAL.  
 FT TRANSMEM 384 404  
 FT SEQUENCE 435 AA; 48571 MW; C964157F CRC32;  
 Query Match 87.0%; Score 47; DB 1; Length 435;  
 Best Local Similarity 87.5%; Pred. No. 2.47e+00;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 13 DYNLTSS 20  
 QY 90 DYSLTSS 97  
 RESULT 11  
 ID TCFH.SCHPO STANDARD; PRT; 558 AA.  
 AC P87153;  
 DT 15-JUL-1998 (REL. 36, CREATED)  
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)  
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
 DE PROBABLE T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA).  
 CCCT7 OR SPEC25H2.12C.  
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972;  
 RA DURSO G., LYE G., BOWMAN S., CHURCH C., WOOD V., BARRELL B.G.,  
 RA RAJANDREAM M.A., CONNOR R.E.;  
 RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 CC -1- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON  
 ATP HYDROLYSIS. KNOWN TO PLAY A ROLE IN VITRO, IN THE FOLDING OF  
 ACTIN AND TUBULIN (BY SIMILARITY).  
 CC -1- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 KD THAT  
 CC FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).  
 CC -1- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.  
 DR EMBL: Z95397; E315886; -.  
 DR PROSITE: P500750; TCP1\_1; 1.  
 DR PROSITE: P500751; TCP1\_2; 1.  
 DR PROSITE: P500995; TCP1\_3; 1.  
 KW CHAPERONE; ATP-BINDING; MULTIGENE FAMILY.  
 SQ SEQUENCE 558 AA; 60686 MW; 0A27A3C4 CRC32;  
 Query Match 87.0%; Score 47; DB 1; Length 558;  
 Best Local Similarity 87.5%; Pred. No. 2.47e+00;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 427 DYSLTSSG 434  
 QY 90 DYSLTSS 97  
 RESULT 12  
 ID KV6C.MOUSE STANDARD; PRT; 107 AA.  
 AC P01677;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-VI REGION (TEPC 601 AND TEPC 191).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE (TEPC 601).  
 RX MEDLINE: 79082830.  
 RA RAO D.N., RUDIKOFF S., POTTER M.;  
 RL BIOCHEMISTRY 17:555-559 (1978).  
 RN [2]  
 RP SEQUENCE (TEPC 191).  
 RX MEDLINE: 81054757.  
 RA RUDIKOFF S., RAO D.N., GLAUDEMANS C.P.J., POTTER M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 77:4270-4274 (1980).  
 CC -1- THE TWO SEQUENCES ARE IDENTICAL.  
 CC -1- THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS THAT BIND  
 GALACTAN.  
 DR PIR: A01941; KVMSX4.  
 DR HSS: P01679; 2FBJ.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 34 48 FRAMEWORK 2.  
 FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 56 87 FRAMEWORK 3.  
 FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 97 106 FRAMEWORK 4.  
 FT DISULFID 23 87 BY SIMILARITY.  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11568 MW; 154F572 CRC32;  
 Query Match 85.2%; Score 46; DB 1; Length 107;  
 Best Local Similarity 77.8%; Pred. No. 4.26e+00;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Db 68 TSYSLTSS 76  
 : |||||

QY 89 SDYSLTSS 97

RESULT 13  
ID KV6D\_MOUSE STANDARD; PRT; 107 AA.

AC P01678;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN V-VI REGION (SAPC 10).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE.

RX MEDLINE: 81054757.

RA RUDIKOFF S., RAO D.N., GLAUDEMANS C.P.J., POTTER M.;

RL PROC. NATL. ACAD. SCI. U.S.A. 77:4270-4274(1980).

CC -1- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.

DR PIR: A01941; KYMSX4.

HSSP: P01679; 2FBJ.

KW IMMUNOGLOBULIN V REGION.

FT DOMAIN 1

FT DOMAIN 2

FT DOMAIN 3

FT DOMAIN 4

FT DOMAIN 5

FT DOMAIN 6

FT DOMAIN 7

FT DOMAIN 8

FT DOMAIN 9

FT DOMAIN 10

FT DOMAIN 11

FT DOMAIN 12

FT DOMAIN 13

FT DOMAIN 14

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FT DOMAIN 38

FT DOMAIN 39

FT DOMAIN 40

FT DOMAIN 41

FT DOMAIN 42

Best Local Similarity 77.8%; Pred. No. 4.26e+00;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 68 TSYSLTSS 76

QY 89 SDYSLTSS 97

RESULT 15  
ID KV6B\_MOUSE STANDARD; PRT; 107 AA.

AC P01676;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN V-VI REGION (XRPC 24).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE.

RX MEDLINE: 79082830.

RA RAO D.N., RUDIKOFF S., POTTER M.;

RL BIOCHEMISTRY 17:5555-5559(1978).

CC -1- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.

DR PIR: A01941; KYMSX4.

HSSP: P01679; 2FBJ.

KW IMMUNOGLOBULIN V REGION.

FT DOMAIN 1

FT DOMAIN 2

FT DOMAIN 3

FT DOMAIN 4

FT DOMAIN 5

FT DOMAIN 6

FT DOMAIN 7

FT DOMAIN 8

FT DOMAIN 9

FT DOMAIN 10

FT DOMAIN 11

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FT DOMAIN 34

FT DOMAIN 35

FT DOMAIN 36

FT DOMAIN 37

FT DOMAIN 38

Best Local Similarity 77.8%; Pred. No. 4.26e+00;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 68 TSYSLTSS 76

QY 89 SDYSLTSS 97

RESULT 15  
ID KV6B\_MOUSE STANDARD; PRT; 107 AA.

AC P01676;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN V-VI REGION (XRPC 24).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE.

RX MEDLINE: 79082830.

RA RAO D.N., RUDIKOFF S., POTTER M.;

RL BIOCHEMISTRY 17:5555-5559(1978).

CC -1- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.

DR PIR: A01941; KYMSX4.

HSSP: P01679; 2FBJ.

KW IMMUNOGLOBULIN V REGION.

FT DOMAIN 1

FT DOMAIN 2

FT DOMAIN 3

FT DOMAIN 4

FT DOMAIN 5

FT DOMAIN 6

FT DOMAIN 7

FT DOMAIN 8

FT DOMAIN 9

FT DOMAIN 10

FT DOMAIN 11

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FT DOMAIN 36

FT DOMAIN 37

FT DOMAIN 38

Search completed: Tue Apr 20 14:07:25 1999  
Job time : 5 secs.

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RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C:
RA UDA T., HIFUMI E., ISHIMARU M., MORIHARA F., ITOH T.:
RL J. FERMENT. BIOENG. 83:333-340(1997).
DR EMBL: D55701; D1024447; -.
DR EMBL: D86361; D1024550; -.
DR PFAM: PF00047; 19.
FT NON_TER 1 1
SQ SEQUENCE 107 AA; 11933 MW; 3BF775AC CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.61e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 DYSLTISS 77
11111111
90 DYSLTISS 97

RESULT 3
ID 015358 PRELIMINARY; PRT; 117 AA.
AC 015358;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE IMMUNOGLOBULIN VARIABLE REGION, KAPPA LIGHT CHAIN (FRAGMENT).
GN VLA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA JUTUL L., HODGS L., BARRINGTON T.:
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: Y14865; E1169998; -.
DR PFAM: PF00047; 19.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12748 MW; 034081EF CRC32;

Query Match
Best Local Similarity 77.8%; Score 50; DB 4; Length 117;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

91 TDYTLTISS 99
11111111
89 SDYSLTISS 97

RESULT 4
ID 090478 PRELIMINARY; PRT; 1197 AA.
AC 090478;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE ADESION MOLECULE L1.1 (FRAGMENT).
OS BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96155762.
RA TONGIORGI E., BERNHARDT R.R., SCHACHNER M.:
RL EMBL: X89204; G1065714; -.
DR PFAM: PF00041; fn3.
DR PFAM: PF00047; 19.
FT NON_TER 1 1
SQ SEQUENCE 1197 AA; 132860 MW; 6D9423C0 CRC32;

Query Match
Best Local Similarity 66.7%; Pred. No. 4.54e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 825 SDYTLTITA 833
11111111
89 SDYSLTISS 97

RESULT 5
ID 058025 PRELIMINARY; PRT; 787 AA.
AC 058025;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DE 787A LONG HYPOTHETICAL PROTEIN.
GN PHB045.
OS PYROCOCCUS HORIKOSHII.
OC ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RA KAWABAYASHI Y., SAWADA M., HORIKAWA H., HAIKANA Y., HINO Y.,
RA YAMAMOTO S., SEKINE M., BABI S., KOSUGI H., HOSOIYAMA A., NAGAI Y.,
RA SAKAI M., OGURA K., OTSUKA R., NAKAZAWA H., TAKAMITA M., OHFUKU Y.,
RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA AOKI K., YOSHIZAWA T., NAKAMURA Y., MASUCHI Y., SHIZUYA H., KIKUCHI H.:
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AB009473; D1027408; -.
SQ SEQUENCE 787 AA; 86903 MW; B47F09A6 CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.25e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 564 SDYSLTI 570
11111111
89 SDYSLTI 95

RESULT 6
ID 016077 PRELIMINARY; PRT; 93 AA.
AC 016077;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE RHEUMATOID FACTOR KAPPA CHAIN VJ REGION (FRAGMENT).
GN RF-VKAPPA>1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94033036.
RA MARTIN T., CROUZIER R., BLAISON G., LEVALLOIS H., PASOUALI J.L.:
RL AUTOIMMUNITY 15:163-170(1993).
DR EMBL: S67059; E98153; -.
DR PFAM: PF00047; 19.
FT NON_TER 1 1
SQ SEQUENCE 93 AA; 10082 MW; 3A915983 CRC32;

Query Match
Best Local Similarity 66.7%; Score 45; DB 4; Length 93;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 54 TDFTLTISS 62
11111111
89 SDYSLTISS 97

RESULT 7
ID 016078 PRELIMINARY; PRT; 93 AA.
AC 016078;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

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DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE RE-V KAPPA 1-RHEUMATOID FACTOR V KAPPA REGION (CLONE SLK77)
DE (FRAGMENT).
CN RE-V(KAPPA>1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 9403036.
RA MARTIN T., CROUZIER R., BLAISON G., LEVALLOIS H., PASQUALI J.L.;
RL AUTOIMMUNITY 15:163-170(1993).
DR EMBL: S67060; E98154; -.
DR PFM: PF00047; 1g.
FT NON_TER 1 1
FT NON_TER 93 93
SQ SEQUENCE 93 AA; 10178 MW; 610B33C1 CRC32;

Query Match
Best Local Similarity 66.7%; Score 45; DB 4; Length 93;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 54 TDFLTISS 62
OY 89 SDYSLTISS 97

RESULT 8
ID 099514 PRELIMINARY; PRT; 105 AA.
AC 099514;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE LIGHT CHAIN FAB FRAGMENT (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA HORN M.P., VOGEL M., BINGI C., MIESCHER S.M., STADLER B.M.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: Y08148; E274854; -.
DR PFM: PF00047; 1g.
FT NON_TER 1 1
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11303 MW; 249B7EC3 CRC32;

Query Match
Best Local Similarity 83.3%; Score 45; DB 4; Length 105;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 67 TDFLTISS 75
OY 89 SDYSLTISS 97

RESULT 9
ID 09953 PRELIMINARY; PRT; 107 AA.
AC 09953;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE VASOACTIVE INTESTINAL POLYPEPTIDE HYDROLYZING AUTOANTIBODY LIGHT CHAIN
DE (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96375171.
RA TYUTYUKOVA S., GAO Q.S., THOMPSON A., RENNARD S., PAUL S.;
RL BIOCHIM. BIOPHYS. ACTA 1316:217-223(1996).

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DR EMBL: I43499; G1850134; -.
DR PFM: PF00047; 1g.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11468 MW; 3D1FE15 CRC32;

Query Match
Best Local Similarity 66.7%; Score 45; DB 4; Length 107;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 69 TDFLTISS 77
OY 89 SDYSLTISS 97

RESULT 10
ID 014540 PRELIMINARY; PRT; 113 AA.
AC 014540;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE HRV FAB 027-VL (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PBL.
RA ITOH K., SUZUKI T.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AB006849; D1023047; -.
DR PFM: PF00047; 1g.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12383 MW; FCEB1F02 CRC32;

Query Match
Best Local Similarity 66.7%; Score 45; DB 4; Length 113;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 71 TDFLTISS 79
OY 89 SDYSLTISS 97

RESULT 11
ID 014535 PRELIMINARY; PRT; 113 AA.
AC 014535;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE HRV FAB N6-VL (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PBL.
RA ITOH K., SUZUKI T.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AB006842; D1023041; -.
DR PFM: PF00047; 1g.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12207 MW; A546C704 CRC32;

Query Match
Best Local Similarity 66.7%; Score 45; DB 4; Length 113;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 71 TDFLTISS 79
OY 89 SDYSLTISS 97

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RESULT 12
ID 039826 PRELIMINARY; PRT; 115 AA.
AC 039826;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE ANTI-HIV-1 GP120 V3 LOOP ANTIBODY D0142-10 LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA DITZEL H.J., PAREN P.W.H.I., BINLEY J.M., SODROSKI J., MOORE J.P.,
RA BARBAS C.F., BURTON D.R.;
RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U82962; G1800287; -.
SQ NON_TER 1
NON_TER 115 1
SEQUENCE 115 AA; 12740 MW; 745D103A CRC32;

Query Match
Best Local Similarity 66.7%; Score 45; DB 4; Length 115;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 75 TDFTLTISS 83
QY 89 SDYSLTISS 97

RESULT 13
ID 015986 PRELIMINARY; PRT; 118 AA.
AC 015986;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE RHEUMATOID FACTOR D5 LIGHT CHAIN (FRAGMENT).
GN V<KAPPA>3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA ERMEL R.W., KENNY T.P., CHEN P.P., ROBBINS D.L.;
RL ARTHRITIS RHEUM. (MUNCH.) 36:380-388(1993).
DR EMBL: S56199; G298553; -.
PRAM; PF00047; 19.
FT NON_TER 1
NON_TER 118 1
SEQUENCE 118 AA; 12766 MW; D2815206 CRC32;

Query Match
Best Local Similarity 66.7%; Score 45; DB 4; Length 118;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 69 TDFTLTISS 77
QY 89 SDYSLTISS 97

RESULT 14
ID 043690 PRELIMINARY; PRT; 239 AA.
AC 043690;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE ANTI-MPL SCFV (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.

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RA GODDARD A., YUAN J., ZHU Z., CARTER P.;
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF048775; G2911502; -.
FT NON_TER 1
NON_TER 239 1
SEQUENCE 239 AA; 25262 MW; 5B9ABF4C CRC32;

Query Match
Best Local Similarity 66.7%; Score 45; DB 4; Length 239;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 201 TDFTLTISS 209
QY 89 SDYSLTISS 97

RESULT 15
ID 000289 PRELIMINARY; PRT; 240 AA.
AC 000289;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE SINGLE-CHAIN FV FRAGMENT (FRAGMENT).
GN SCFV.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA KONTERMANN R.E., WING M.G., WINTER G.;
RL NAT. BIOTECHNOL. 15:629-631(1997).
DR EMBL: Y13056; E315281; -.
PRAM; PF00047; 19.
FT NON_TER 1
NON_TER 240 1
SEQUENCE 240 AA; 25569 MW; 6472A9C9 CRC32;

Query Match
Best Local Similarity 66.7%; Score 45; DB 4; Length 240;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 201 TDFTLTISS 209
QY 89 SDYSLTISS 97

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Search completed: Tue Apr 20 14:08:04 1999  
Job time : 20 secs.



SQ Sequence 90 AA:

Query Match 100.0%; Score 28; DB 16; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 lsasl 7  
 |||||  
 QY 31 LSASL 35

RESULT 2  
 ID R80079 standard; Protein; 90 AA.  
 AC R80079;

DT 22-MAY-1996 (first entry)  
 DE Mouse derived light chain RT3 phage antibody pattern C.  
 KW Light chain; RT3; murine; catalytic antibody; bacteriophage;  
 pattern C.  
 Mus musculus.

Key Location/Qualifiers  
 FT region 1..15 /note= "framework region 1"  
 FT region 16..26 /note= "complementarity determining region 1"  
 FT region 27..40 /note= "framework region 2"  
 FT region 41..47 /note= "complementarity determining region 2"  
 FT region 48..78 /note= "framework region 3"  
 FT region 79..88 /note= "complementarity determining region 3"  
 FT region 89..90 /note= "framework region 4  
 N-terminal fragment"

W09527045-A1.  
 PD 12-OCT-1995.  
 PF 30-MAR-1994; U03420.  
 PR 30-MAR-1994; WO-U03420.  
 PA (IGEN-); IGEN INC.  
 PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;  
 PI Martin W, Mcclafferty J, Smith RG, Tiltman RC, Williams RO;  
 DR N-PSDB; T04626.  
 PT Production of catalytic antibodies displayed on phage - by  
 generating a gene library of antibody-derived domains and expressing  
 it in phage vectors.  
 CC Disclosure: Fig 9; 133pp; English.  
 CC T04626 encodes R80079 mouse derived light chain RT3 phage antibody.  
 CC The DNA was used in the prepn. of catalytic antibody (CA) producing  
 CC bacteriophage. The CAs can be used to activate/deactivate a  
 CC biological function in an animal by enhancing the rate of cleavage,  
 CC or formation of a specific bond within a mol. in vivo.  
 SQ Sequence 90 AA;

Query Match 100.0%; Score 28; DB 16; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 lsasl 7  
 |||||  
 QY 31 LSASL 35

RESULT 3  
 ID R81328 standard; Protein; 106 AA.  
 AC R81328;

DT 02-APR-1996 (first entry)  
 DE Mouse anti-VLA-4 antibody 21.6 light chain variable region.  
 KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;  
 KM antibody engineering.  
 OS Mus musculus.  
 FH Key Location/Qualifiers

FT region 1..23 /label= FR1  
 FT /note= "mouse light chain variable framework  
 FT region 1"  
 FT 24..34 /label= CDR1  
 FT /note= "mouse light chain variable complementarity  
 FT determining region 1"  
 FT 35..49 /label= FR2  
 FT /note= "mouse light chain variable framework  
 FT region 2"  
 FT 50..56 /label= CDR2  
 FT /note= "mouse light chain variable complementarity  
 FT determining region 2"  
 FT 57..88 /label= FR3  
 FT /note= "mouse light chain variable framework  
 FT region 3"  
 FT 89..96 /label= CDR3  
 FT /note= "mouse light chain variable complementarity  
 FT determining region 3"  
 FT 97..106 /label= FR4  
 FT /note= "mouse light chain variable framework  
 FT region 4"

W09519790-A1.  
 PD 27-JUL-1995.  
 PF 25-JAN-1995; U01219.  
 PR 25-JAN-1994; US-186269.  
 PA (ATHE-) ATHENA NEUROSCIENCES INC.  
 PI Bendig MM, Jones TS, Leger OJ, Saldanha J;  
 DR WPI; 95-269276/35.  
 PT New humanised antibodies against VLA-4 - used for inhibiting  
 PT leukocyte adhesion to endothelial cells, partic. for treating  
 PT inflammatory disease.  
 PS Disclosure: Page 66; 105pp; English.  
 CC The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain  
 CC variable region (without signal sequence). Cloned cDNA CDR sequences of  
 CC mouse 21.6 variable light and variable heavy regions are linked to human  
 CC constant framework regions of the REI antibody for the light chain and  
 CC the 2\*Cl antibody for the heavy chain in the construction of a humanized  
 CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are  
 CC modified using PCR primers (See Q99895-98) and then subcloned into  
 CC mammalian cell expression vectors containing human kappa or gamma-1  
 CC constant regions. In the humanized light chain, amino acids L45, L49,  
 CC L58 and L69 in the human kappa IGV framework are replaced by the amino  
 CC acid present in the equivalent position of the mouse 21.6 Ig light chain.  
 CC Plasmids encoding the chimeric antibodies are transfected into COS cells.  
 CC The humanized antibodies can be used to inhibit adhesion of a leukocyte  
 CC to an endothelial cell and to treat inflammatory diseases such as  
 CC multiple sclerosis. They can also be used in the treatment of stroke,  
 CC cerebral traumas, meningitis or encephalitis. The antibodies can also be  
 CC used for detecting VLA-4, for affinity purification or for generating  
 CC anti-idiotypic antibodies.  
 SQ Sequence 106 AA;

Query Match 100.0%; Score 28; DB 15; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 lsasl 15  
 |||||  
 QY 31 LSASL 35

RESULT 4  
 ID W27121 standard; Protein; 107 AA.  
 AC W27121;

DT 04-JAN-1998 (first entry)  
 DE Murine antibody light chain variable region consensus.

KW Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;  
 OS human milk fat globule; HMEG; tumour; breast cancer; vaccine.  
 FT Mus musculus.  
 FT Key  
 FT Region  
 FT Location/Qualifiers  
 FT 24..34  
 FT /label= CDR1  
 FT /note= "complementarity determining region 1"  
 FT 50..56  
 FT /label= CDR2  
 FT /note= "complementarity determining region 2"  
 FT 88..96  
 FT /label= CDR3  
 FT /note= "complementarity determining region 3"  
 FT Region  
 FT W09722699-A2.  
 PD 26-JUN-1997.  
 PF 19-DEC-1996; U20757.  
 PR 13-DEC-1996; US-575762.  
 PR 20-DEC-1995; US-575762.  
 PR 26-JAN-1996; US-591965.  
 PR (KENT) UNIV KENTUCKY.  
 PR Chatterjee M, Chatterjee SK, Foon KA;  
 WPI: 97-341690/31.  
 PT Monoclonal anti-idiotypic antibody 11D10 - elicits immune response  
 PT against human milk fat globule disease associated tumours,  
 PT especially breast cancer.  
 PS Example 2; Fig 26C; 130pp; English.  
 CC This polypeptide sequence comprises a consensus sequence of murine  
 CC light chain variable regions (VL) selected on the basis of identity  
 CC to the VL region (see W27119) of monoclonal anti-idiotypic antibody  
 CC 11D10. The sequences were obtained from a Genbank database  
 CC search. A VH consensus (W27122) was also produced. 11D10 has at  
 CC least 18 departures from the consensus sequences (7 in the light  
 CC chain and 11 in the heavy chain). 8 occur within CDRs and 10  
 CC outside CDRs. 11D10 polypeptides and polynucleotides can be  
 CC used in vaccines and pharmaceutical compositions for the treatment  
 CC of human milk fat globule-associated diseases such as breast  
 CC cancer.  
 SO Sequence 107 AA;  
 Query Match 100.0%; Score 28; DB 25; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 11 lsasl 15  
 Oy 31 LSASL 35  
 UTL 5  
 R27499 standard; protein; 107 AA.  
 AC R27499; 1993 (first entry)  
 DE WNI 222-5 antibody light chain variable domain.  
 KW Monoclonal antibody; Mab; epitope; core region; LPS;  
 KW lipopolysaccharide; endotoxaemia; WNI 222-5; WNI 58-9;  
 KW light; heavy; Gram-negative bacteria.  
 OS Mus musculus.  
 FT Key  
 FT Location/Qualifiers  
 FT 1..23  
 FT /label= 1FR1  
 FT 24..34  
 FT /label= 1CDR1  
 FT 35..49  
 FT /label= 1FR2  
 FT 50..56  
 FT /label= 1CDR2  
 FT 57..88  
 FT /label= 1FR3  
 FT 89..97  
 FT /label= 1CDR3  
 FT 98..107  
 FT /label= 1FR4  
 FT region  
 PD W09216624-A.

PD 01-OCT-1992.  
 PF 22-FEB-1992; E00380.  
 PR 13-MAR-1991; GB-005292.  
 PA (SANO) SANDOZ LTD.  
 PA (SANO) SANDOZ PATENT GMBH.  
 PI Barclay GR, Di Padova F, Gram H, Poxton IR;  
 DR WPI: 92-349209/42.  
 DR N-PSDB: 029150.  
 PT Monoclonal antibodies against LPS core epitope(s) of  
 PT Gram-negative bacteria - for diagnosing, preventing and treating  
 PT Gram-negative bacterial infections  
 PS Claim 23; Page 56 + 43; 82pp; English.  
 CC Monoclonal antibodies which recognise an epitope in the core region  
 CC of the bacterial lipopolysaccharide (LPS) mol. and which are cross-  
 CC protective against endotoxaemia caused by at least two different  
 CC Gram-negative bacterial strains having different core structures,  
 CC pref. comprise the heavy chain variable domain having the sequence  
 CC of R27497 (WNI 222-5) or R27498 (WNI 58-9) and the light chain  
 CC variable domain having the sequence of R27499 (WNI 222-5)  
 CC or R27500 (WNI 58-9).  
 SO Sequence 107 AA;  
 Query Match 100.0%; Score 28; DB 5; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 11 lsasl 15  
 Oy 31 LSASL 35  
 RESULT 6  
 ID R30768 standard; protein; 107 AA.  
 AC R30768; 1993 (first entry)  
 DE Murine anti-CD3 Mab UCHL1 light chain variable domain.  
 KW Humanisation; rapid; monoclonal antibody; muxeD3.  
 OS Mus musculus.  
 PN W09222653-A.  
 PD 23-DEC-1992; U05126.  
 PF 15-JUN-1992; US-715272.  
 PR 14-JUN-1991; US-715272.  
 PA (GETH) GENENTECH INC.  
 PI Carter PJ, Presta LG;  
 DR WPI: 93-018139/02.  
 FT Humanisation of antibodies - by molecular modelling of the variable  
 FT domains and alteration by gene conversion mutagenesis  
 PS Disclosure; Fig 5; 126pp; English.  
 CC The sequence is that of the light chain variable domain of murine  
 CC anti-CD3 monoclonal antibody UCHL1 (muxeD3, Shalaby 1992).  
 SO Sequence 107 AA;  
 Query Match 100.0%; Score 28; DB 6; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 11 lsasl 15  
 Oy 31 LSASL 35  
 RESULT 7  
 ID W16620 standard; protein; 108 AA.  
 AC W16620; 1998 (first entry)  
 DE Anti-human FasL antibody (NOK1) light chain variable region.  
 KW Light chain; variable region; mouse; murine; human; Fas ligand;  
 KW FasL; monoclonal antibody; Mab; hybridoma; treatment; hepatitis;  
 KW hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis;  
 KW liver cell; glutamate oxaloacetate; pyruvate transaminase.  
 OS Mus sp.  
 PN W09715326-A1.  
 PD 01-MAY-1997.

PF	24-OCT-1996;	J03089.	
PR	27-OCT-1995;	JP-303491.	
PA	(SOME) SUMITOMO ELECTRIC IND CO.		
PI	Kayagaki N, Nakata M, Okumura K, Selno K, Yagita H;		
DR	WPI; 97-28767/23.		
DR	N-PSDB; 7667710.		
PT	Anti-human Fas ligand antibody to treat hepatitis - controls		
PS	apoptosis in liver cells and improves liver function		
PT	Claim 6; Pages 30-31; 51pp; Japanese.		
CC	The present sequence is the light chain variable region of the		
CC	murine anti-human Fas ligand (FasL) monoclonal antibody (Mab) NOKI,		
CC	which is expressed by the hybridoma NOKI (FERM BP-5044). The Mab		
CC	can be used in the preparation of a composition for the effective		
CC	oral or parenteral treatment of hepatitis, including hepatitis		
CC	caused by hepatitis B or C virus. The composition controls apoptosis		
CC	in liver cells caused by the binding of FasL to Fas expressing liver		
CC	cells, and improves liver function by improving blood glutamate		
CC	oxaloacetate and pyruvate transaminase levels. The composition is		
CC	given in a dosage of 0.0001-1000, preferably 0.01-600 mg/day.		
CC	Spleen cells from mice immunised with FasL expressing COS cells		
CC	were fused with mouse myeloma cells to produce hybridomas. The		
CC	hybridomas were screened for anti-FasL activity, and the active		
CC	clones NOKI-5 isolated.		
SQ	Sequence 108 AA;		
	Query Match 100.0%; Score 28; DB 25; Length 108;		
	Best Local Similarity 100.0%; Pred. No. 1.47e+03;		
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
DB	11 lsasl 15		
OY	31 LSASL 35		
RESULT 8			
ID	R93159 standard; Protein; 108 AA.		
AC	R93159;		
DT	24-OCT-1996 (first entry)		
DE	Murine monoclonal antibody K20 kappa chain variable region.		
KW	Antibody; Light chain; Kappa; variable region; K20; Integrin; CD29;		
KW	beta 1 subunit; humanisation; Hu-K20; Immunosuppressant;		
KW	T cell activation; complementarity determining region; CDR.		
OS	Mus musculus.		
FH	Key		
FH	Location/Qualifiers		
FT	region	1..23	
FT	/label= FRI		
FT	/note= "framework region"		
FT	region	24..34	
FT	/label= CDRI		
FT	/note= "complementarity determining region"		
FT	region	35..49	
FT	/label= FR2		
FT	/note= "framework region"		
FT	region	50..56	
FT	/label= CDR2		
FT	/note= "complementarity determining region"		
FT	region	57..88	
FT	/label= FR3		
FT	/note= "framework region"		
FT	region	89..94	
FT	/label= CDR3		
FT	/note= "complementarity determining region"		
FT	region	95..108	
FT	/label= J_kappa1		
FT			
FN	FR2724393-A1.		
PD	15-MAR-1996.		
PR	12-SEP-1994; 010858.		
PR	12-SEP-1994; FR-010858.		
PA	(INRM) INSERM INST NAT SANTE & RECH MEDICALE.		
PI	BERNARD A, CERVOINI MF, LESTRANC MP, MARGARITTE C;		
PI	POUL MA;		
PR	WPI; 96-162083/17.		

DR	N-PSDB: T26849.
CC	Humanisation of non-human immunoglobulin variable regions - for
PT	prodn. of humanised antibodies, esp. K20, e.g. as an
PT	Immunosuppressant
PS	Example 1; Fig 2A; 39pp; French.
CC	The present sequence is that of the variable region of the kappa
CC	light chain from murine monoclonal antibody K20. The antibody
CC	recognises the beta 1 subunit (CD29) of integrins and inhibits
CC	activation and proliferation of peripheral T cells induced by
CC	anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target
CC	for humanisation. In the humanisation process, the complementarity
CC	determining regions (CDRs) of a human antibody with framework
CC	regions 70-95% homologous to those of K20 were replaced by the K20
CC	CDSs.
SQ	Sequence 108 AA:
Query Match	100.0%; Score 28; DB 18; Length 108;
Best Local Similarity	100.0%; Pred. No. 1,47e+03;
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps
Db	11 Isasl 15
Oy	31 LSASL 35
RESULT	9
ID	R21286 standard; Protein: 108 AA.
AC	R21286:
DE	21-MAY-1992 (first entry)
KW	Murine VL kappa group V chain "a", specific for pHOx.
KW	EJ; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW	plus; gsp; binding; adsorption; gene VIII; diverse repertoire;
KV	specific binding pairs; replicable genetic display package.
OS	Synthetic.
FH	Key
FT	binding_site
FT	/label= CDR1
FT	binding_site
FT	/label= CDR2
FT	binding_site
FT	/label= CDR3
FT	/note=" D-X-G-X-X motif "
PN	WO9201047-A.
PD	23-JAN-1992.
PR	10-JUL-1991; GB-015198.
PR	19-OCT-1990; GB-022845.
PR	12-NOV-1990; GB-024503.
PR	06-MAR-1991; GB-004744.
PR	15-MAY-1991; GB-010549.
PA	(CAMP-) CAMBRIDGE ANTIBODY.
PI	(MED1-) MED RES COUNCIL.
P1	McCaferthy J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
P1	Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ,
DR	Milner GP, Bonnett TP;
DR	WPI: 92-056862/07.
PT	Recombinant members of specific binding pairs - by expression in
PT	dominant host cells with a secreting replicable genetic
PT	display package.
PS	Example 21; Fig 24; 209pp; English.
CC	The VK sequence is one of seven (R21286-92) found to be expressed
CC	from a single chain Fv library from an immunised mouse. The library
CC	produces a diverse repertoire of antibody fragments specific for
CC	2-phenyl-5-oxazolone (phox). It was prepd. using cDNA generated
CC	from mRNA from mice immunised with phox coupled to chicked serum
CC	albumin. The VH and VL kappa sequences were separately amplified
CC	by PCR (see Q23474-84) and ligated into fdCAT2 (see Q23463) for ex-
CC	pression on the phage surface as fusions with gene III. The result-
CC	ing library of clones was diverse. Twenty three hapten binding
CC	clones were sequenced revealing eight different VH genes (A-H) (see
CC	R21264-71) in a variety of pairings with the seven different VK
CC	genes (a-g). Of the twenty three clones sequenced, three were of

CC type "a", and were "ox-like" genes. (See Berec et al, Nature 316  
 CC 412-418, 1985). They contain the DX6XX motif in CDR3, the central  
 CC gly of which is needed to create a cavity for phox. Most of the  
 CC clones were VJ-d combinations. The Kd of VH-B/VJ-d for phox-GABA  
 CC was 10 nM. Only two other combinations (of eleven tested) were  
 CC found to have higher values. This suggests that phage bearing scFv  
 CC fragments having weak affinities can be selected with antigen, pro-  
 CC bably due to the avidity of the multiple antibody heads on the  
 CC phage.  
 CC See also R21260-307, 309-311; R22450, 565-581.  
 SQ Sequence 108 AA;

Query Match 100.0%; Score 28; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 11 Isasl 15  
 OY 31 LSASL 35

RESULT 10  
 ID W18270 standard; peptide: 109 AA.  
 AC W18270;  
 DT 09-JAN-1998 (first entry)  
 DE PRP 28 light chain variable region.  
 KW Prion protein; PrP: heavy chain variable region; antibody; scrapie;  
 KW light chain variable region; PrP-Sc; pathogen; fatal familial insomnia;  
 KW central nervous system spongiform encephalopathy; human; therapy;  
 KW transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease;  
 KW bovine spongiform encephalopathy; feline spongiform encephalopathy;  
 KW Serstmann-strassler-scheinker Disease.  
 OS Mus musculus.  
 FH Key  
 FT Location/Qualifiers  
 FT 1..23  
 FT /note= "framework region 1"  
 FT 24..34  
 FT /note= "complementarity determining region 1"  
 FT 35..49  
 FT /note= "framework region 2"  
 FT 50..56  
 FT /note= "complementarity determining region 2"  
 FT 57..88  
 FT /note= "framework region 3"  
 FT 89..97  
 FT /note= "complementarity determining region 3"  
 FT 98..109  
 FT /note= "framework region 4"  
 WO9710505-A1.  
 PD 20-MAR-1997.  
 PF 13-SEP-1996; U14840.  
 PR 14-SEP-1995; US-528104.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Burton DR, Prusiner SB, Williamson RA;  
 DR WPI: 97-202357/18.  
 PT New antibodies to the scrapie isoform of prion protein - used for  
 PT detection of infectious prion proteins or for treating disease such  
 PT as BSE, CJD or scrapie.  
 PS Example 9; Fig 6; 95pp; English.  
 CC W18266-W18285 represent portions of the antibody of the invention. The  
 CC antibodies of the invention are able to bind the scrapie isoform of prion  
 CC protein PrP-Sc in situ. Prions are infectious pathogens that cause  
 CC central nervous system spongiform encephalopathies in humans and animals.  
 CC The scrapie isoform of the prion protein (PrP-Sc) is necessary for both  
 CC the transmission and pathogenesis of the transmissible neurodegenerative  
 CC diseases of animals and humans. The antibodies can be used in a method of  
 CC the invention for detecting human PrP-Sc in a source. The antibodies  
 CC specifically bind to prion proteins associated with disease and do not  
 CC bind to denatured PrP proteins not associated with disease. They can bind  
 CC to prion proteins of a specific species of mammals. They can also have  
 CC the ability to neutralise infectious prions. The antibodies can be used  
 CC for screening for the presence of prions in products such as  
 CC pharmaceuticals, food or cosmetics. They can also be used for prion

CC neutralisation to purify products, for extraction of prion proteins or  
 CC for therapy, for diseases such as bovine spongiform encephalopathy,  
 CC Creutzfeldt-Jakob Disease, fatal familial insomnia or  
 CC Serstmann-strassler-scheinker Disease, scrapie or feline spongiform  
 CC encephalopathies.  
 SQ Sequence 109 AA;

Query Match 100.0%; Score 28; DB 25; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 11 Isasl 15  
 OY 31 LSASL 35

RESULT 11  
 ID W22409 standard; Protein: 126 AA.  
 AC W22409;  
 DT 08-DEC-1997 (first entry)  
 DE Alpha-4 integrin mouse Mab 21.6 VL region.  
 KW Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;  
 KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;  
 KW metastasis; inflammatory bowel disease; rheumatoid arthritis;  
 KW transplant rejection; graft versus host disease; nephritis;  
 KW atopic dermatitis; psoriasis; myocardial ischaemia;  
 KW acute leukocyte mediated lung injury; therapy.  
 OS Mus musculus.  
 FH Key  
 FT Location/Qualifiers  
 FT peptide  
 FT 1..20  
 FT /label= Leader  
 FT 21..43  
 FT /note= "framework region 1"  
 FT 44..54  
 FT /label= CDR1  
 FT 55..69  
 FT /note= "complementarity determining region 1"  
 FT 70..76  
 FT /label= FR2  
 FT /note= "framework region 2"  
 FT 77..108  
 FT /label= CDR2  
 FT /note= "complementarity determining region 2"  
 FT 109..116  
 FT /label= FR3  
 FT /note= "framework region 3"  
 FT 117..126  
 FT /label= CDR3  
 FT /note= "complementarity determining region 3"  
 FT 127..126  
 FT /label= FR4  
 FT /note= "framework region 4"  
 WO9718838-A1.  
 PD 29-MAY-1997.  
 PF 21-NOV-1996; U18807.  
 PR 21-NOV-1995; US-561521.  
 PA (ATHE-) ATHENA NEUROSCIENCES INC.  
 PI Bendig MW, Jones ST, Leger OJ, Saldanha J, Yednock TA;  
 DR WPI: 97-297879/27.  
 DR N-PSDB: T74759.  
 PT Uses of humanised alpha-4 integrin antibody - for treatment of  
 PT asthma, atherosclerosis, AIDS, dementia, etc.  
 PS Claim 18; Page 68; 107pp; English.  
 CC This polypeptide comprises the light chain variable region (VL) of  
 CC mouse anti-alpha-4 integrin monoclonal antibody 21.6. The  
 CC complementarity determining regions (CDRs) of the 21.6 VL can be  
 CC incorporated into a human RFI framework to produce a claimed  
 CC humanised 21.6 VL (see W22412) and a claimed humanised 21.6  
 CC antibody that is used in the manufacture of a medicament for  
 CC treating a disease selected from asthma, atherosclerosis, AIDS,  
 CC dementia, diabetes, inflammatory bowel disease, rheumatoid  
 CC arthritis, transplant rejection, graft versus host disease, tumour  
 CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial

CC ischaemia, and acute leukocyte mediated lung injury. The antibody  
CC may also be used in the affinity purification of alpha-4 integrin  
CC for use as a vaccine or an immunogen. It is also useful for  
CC generating idiotype antibodies. The humanized antibodies of the  
CC invention have a half-life in the human circulation essentially  
CC equivalent to that of naturally occurring human antibodies.  
SQ Sequence 126 AA;

Query Match 100.0%; Score 28; DB 24; Length 126;  
Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 lsasl 35  
|||||  
Qy 31 LSASL 35

RESULT 12  
R81332 standard; Protein; 126 AA.  
R81332:

DE 23-MAR-1996 (first entry)  
KW Human VLA-4 reshaped antibody 21.6 light chain variable region.  
OS Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;  
FH Key  
FT peptide  
FT location/Qualifiers  
FT 1..20  
FT /note- "signal peptide"  
FT 21..43  
FT /note- "framework region 1"  
FT 44..54  
FT /note- "complementarity determining region 1"  
FT 55..69  
FT /note- "framework region 2"  
FT 70..76  
FT /note- "complementarity determining region 2"  
FT 77..108  
FT /note- "framework region 3"  
FT 109..116  
FT /note- "complementarity determining region 3"  
FT 117..126  
FT /note- "framework region 4"

WO9519790-A1.

27-JUL-1995.

25-JAN-1995; U01219.

25-JAN-1994; US-186269.

(ATHE-) ATHENA NEUROSCIENCES INC.  
Bending MM, Jones TS, Leger OJ, Saldaña J;  
N-PSDB; Q99893.

PT New humanised antibodies against VLA-4 - used for inhibiting  
PT leukocyte adhesion to endothelial cells, partic. for treating  
PT inflammatory disease.

PS Disclosure: Fig 10; 105pp; English.

CC The sequence represents the human reshaped antibody 21.6 light  
CC chain variable region against leukocyte adhesion molecule VLA-4.

CC Cloned CDNA sequences of mouse 21.6 VL (Q99893) and VH (Q99892)  
CC of a humanized antibody against VLA-4. The 5' and 3' ends of the  
CC mouse CDNA are modified using PCR primers (See Q99895-98) and

CC then subcloned into mammalian cell expression vectors containing  
CC human kappa or gamma-1 constant regions. In the humanized light  
CC chain, amino acids L45, L49, L58 and L69 in the human kappa IC VR

CC framework are replaced by the amino acid present in the equivalent  
CC position of the mouse 21.6 Ig L chain. Plasmids encoding the  
CC chimeric antibodies are transfected into COS cells. The humanized

CC antibodies can be used to inhibit adhesion of a leukocyte to an  
CC endothelial cell and to treat inflammatory diseases such as

CC multiple sclerosis. They can also be used in the treatment of  
CC stroke, cerebral trauma, meningitis or encephalitis. The

CC antibodies can also be used for detecting VLA-4, for affinity  
CC purification or for generating anti-idiotypic antibodies.

SQ Sequence 126 AA;

Query Match 100.0%; Score 28; DB 15; Length 126;  
Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 lsasl 35  
|||||  
Qy 31 LSASL 35

RESULT 13  
ID R81326 standard; Protein; 126 AA.  
AC R81326;  
DT 23-MAR-1996 (first entry)

DE Mouse VLA-4 antibody 21.6 light chain variable region.  
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;  
OS Mus musculus.  
FH Key  
FT peptide  
FT location/Qualifiers  
FT 1..20  
FT /note- "signal peptide"  
FT 21..43  
FT /note- "framework region 1"  
FT 44..54  
FT /note- "complementarity determining region 1"  
FT 55..69  
FT /note- "framework region 2"  
FT 70..76  
FT /note- "complementarity determining region 2"  
FT 77..108  
FT /note- "framework region 3"  
FT 109..116  
FT /note- "complementarity determining region 3"  
FT 117..126  
FT /note- "framework region 4"

WO9519790-A1.

27-JUL-1995.

25-JAN-1995; U01219.

25-JAN-1994; US-186269.

(ATHE-) ATHENA NEUROSCIENCES INC.  
Bending MM, Jones TS, Leger OJ, Saldaña J;  
N-PSDB; Q99893.

PT New humanised antibodies against VLA-4 - used for inhibiting  
PT leukocyte adhesion to endothelial cells, partic. for treating  
PT inflammatory disease.

PS Disclosure: Fig 1; 105pp; English.

CC The sequence represents the mouse antibody 21.6 light chain variable  
CC region directed against leukocyte adhesion molecule VLA-4. Cloned  
CC CDNA sequences of mouse 21.6 VL and VH (see Q99892) regions are

CC linked to human constant regions in the construction of a humanized  
CC antibody against VLA-4. The 5' and 3' ends of the mouse CDNA are

CC modified using PCR primers (See Q99895-98) and then subcloned into  
CC mammalian cell expression vectors containing human kappa or gamma-1

CC constant regions. In the humanized light chain, amino acids L45,  
CC L49, L58 and L69 in the human kappa IC VR framework are replaced

CC by the amino acid present in the equivalent position of the mouse  
CC 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are

CC transfected into COS cells. The humanized antibodies can be used  
CC to inhibit adhesion of a leukocyte to an endothelial cell and

CC to treat inflammatory diseases such as multiple sclerosis. They  
CC can also be used in the treatment of stroke, cerebral trauma,

CC meningitis or encephalitis. The antibodies can also be used for  
CC detecting VLA-4, for affinity purification or for generating

CC anti-idiotypic antibodies.

SQ Sequence 126 AA;

Query Match 100.0%; Score 28; DB 15; Length 126;  
Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 lsasl 35  
|||||



QY 31 LSASL 35

RESULT 14  
 ID R12237 standard; Protein; 126 AA.  
 AC R12237;  
 DT 19-AUG-1991 (first entry)  
 DE Mouse Mab 1C11 L chain V region.  
 KM HIV-1; chimera.  
 OS Mus sp.  
 PN WO9107494-A.  
 PD 30-MAY-1991.  
 PE 13-NOV-1990; U06627.  
 PR 13-NOV-1989; US-433703.  
 PA (XOMA-) Xoma Corp.  
 PI Better MO, Horwitz AH, Ghosh-Dastidar P, Robinson RR;  
 DR WPI: 91-178106/24.  
 DR N-PSDB: 012017.  
 PT New chimeric mouse human antibodies - used in treatment, diagnosis  
 and prophylaxis of HIV infections.  
 CC Disclosure; Fig 13; 108pp; English.  
 CC The mouse VL gene product may be used to produce chimeric mouse-  
 human Abs against HIV-1 comprising human Ig constant regions and  
 murine variable regions. These novel sequence are useful in  
 CC treatment, diagnosis and prophylaxis of HIV infections, and may be  
 CC produced by a bacterial, yeast or mammalian expression system.  
 SQ Sequence 126 AA;

Query Match 100.0%; Score 28; DB 2; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 LSASL 35  
 QY 31 LSASL 35

RESULT 15  
 ID R99003 standard; Protein; 127 AA.  
 AC R99003;  
 DT 10-JAN-1997 (first entry)  
 DE Mab V17E6 light chain (specific for human alphaV integrins).  
 KM Monoclonal antibody; Mab; integrin; cell-matrix interaction.  
 KW tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2; IL-2;  
 OS Mus musculus.  
 FH Key location/Qualifiers  
 region 21..43  
 binding\_site /label- Framework region 1  
 region 44..54  
 binding\_site /label- CDRI  
 region 55..69  
 binding\_site /label- Framework region 2  
 region 70..76  
 binding\_site /label- CDR2  
 region 77..108  
 binding\_site /label- Framework region 3  
 region 109..117  
 binding\_site /label- CDR3  
 region 118..127  
 binding\_site /label- Framework region 4  
 EP-719859-A1.  
 PD 03-JUL-1996.  
 PR 06-DEC-1995; 119233.  
 PR 20-DEC-1994; EP-120165.  
 PA (MERE) MERCK PATENT GMBH.  
 PI Aden J, Goodman S, Hahn D, Mitjans F, Pinlats J;  
 PI Rosell E;  
 DR WPI: 96-302345/31.  
 DR N-PSDB: T35050.  
 PT New human integrin V chain-specific monoclonal antibody - and  
 PT related DNA and hybridomas, for treatment and diagnostic imaging of  
 PT tumours, esp melanoma.

PS Claim 8; Figure 17a; 54pp; English.

CC A monoclonal antibody which reacts only with the alphaV chain of  
 CC human alphaV integrins; which blocks attachment of alphaV integrin  
 CC bearing cells to integrin substrate; which reverses established cell  
 CC matrix interactions caused by alphaV integrin; which blocks tumour  
 CC development and which has no cytotoxic activity; may be used to  
 CC treat tumours, especially melanoma (but also glioma, carcinoma)  
 CC optionally coupled to a cytokine such as interleukin-2. The  
 CC monoclonal antibody may also be used for diagnostic imaging of  
 CC tumours and assessment of tumour growth when conjugated to a  
 CC radiolabel or a radio opaque-agent.  
 SQ Sequence 127 AA;

Query Match 100.0%; Score 28; DB 20; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 1.47e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 LSASL 35  
 QY 31 LSASL 35

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
n on: Tue Apr 20 13:56:19 1999; Maspar time 3.21 Seconds  
58.270 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-836-455-2  
Description: (31-35) from US08836455.pep (1 of 3)  
Perfect Score: 28  
Sequence: 1 LSASL 5

Scoring table:  
PAM 150  
Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: plr58  
1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 17.008; Variance 14.078; scale 1.208

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	28	100.0	45	2	S28565	hypothetical protein
2	28	100.0	93	2	S38564	Ig kappa chain V regl
3	28	100.0	102	2	S50530	hypothetical protein
4	28	100.0	106	2	C33936	Ig kappa chain V regl
5	28	100.0	106	2	PI0259	Ig kappa chain V regl
6	28	100.0	106	2	PI0260	Ig kappa chain V regl
7	28	100.0	108	4	B47271	nitrophenyl phosphona
8	28	100.0	108	4	C26405	Ig kappa chain V regl
9	28	100.0	108	4	B26405	Ig kappa chain V regl
10	28	100.0	109	1	KVMS09	Ig kappa chain V regl
11	28	100.0	109	1	KVMS82	Ig kappa chain V regl
12	28	100.0	124	1	S03521	Ig kappa chain precu
13	28	100.0	130	1	KVMSM4	Ig kappa chain precu
14	28	100.0	138	2	B63465	transcription regulat
15	28	100.0	165	2	JE0065	retroviral proteinase
16	28	100.0	177	2	F70508	probable transmembran
17	28	100.0	182	2	C71214	hypothetical protein
18	28	100.0	230	2	S33161	Ig kappa chain - shce
19	28	100.0	245	2	D71554	probable adenylate cy
20	28	100.0	268	2	A70417	hypothetical protein
21	28	100.0	280	2	H71320	hypothetical protein
22	28	100.0	303	2	B47089	probable Arac-type re
23	28	100.0	304	2	E45277	probable transcriptio

Result	Entry	Title	Organism	Accessions	Reference	Journal	Title	Accessions	Reference	Journal	Title
24	28	100.0	307	2	S67662	hypothetical protein	6.56e+02				
25	28	100.0	317	2	S63358	hypothetical protein	6.56e+02				
26	28	100.0	327	1	S26693	transcription factor	6.56e+02				
27	28	100.0	352	2	E71164	hypothetical protein	6.56e+02				
28	28	100.0	354	2	A64894	hypothetical protein	6.56e+02				
29	28	100.0	371	2	C70626	hypothetical protein	6.56e+02				
30	28	100.0	412	2	F64849	probable permease b10	6.56e+02				
31	28	100.0	417	2	S64006	hypothetical protein	6.56e+02				
32	28	100.0	419	2	A70814	probable integral mem	6.56e+02				
33	28	100.0	452	2	S77040	hypothetical protein	6.56e+02				
34	28	100.0	504	2	S24314	bacterial leucyl amin	6.56e+02				
35	28	100.0	551	2	S66701	probable membrane pro	6.56e+02				
36	28	100.0	576	2	B71420	hypothetical protein	6.56e+02				
37	28	100.0	591	2	D64204	membrane lipoprotein	6.56e+02				
38	28	100.0	592	2	S54489	phosphoribosylaminom	6.56e+02				
39	28	100.0	685	2	S64985	hypothetical protein	6.56e+02				
40	28	100.0	709	2	E64213	DNA topoisomerase (EC	6.56e+02				
41	28	100.0	1048	2	S57155	NMD5 protein - yeast	6.56e+02				
42	28	100.0	1150	2	B47114	phosphoprotein phosph	6.56e+02				
43	28	100.0	1671	2	S71628	sensory transduction	6.56e+02				
44	28	100.0	1698	2	S51869	probable membrane pro	6.56e+02				
45	28	100.0	2672	2	A48126	translation activator	6.56e+02				

## ALIGNMENTS

RESULT 1  
ENTRY S28565 #type complete  
TITLE hypothetical protein (Athb-2 5' region) - Arabidopsis thaliana  
ORGANISM #formal\_name Arabidopsis thaliana #common\_name mouse-ear cress  
#variety strain Columbia  
DATE 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 24-Sep-1998  
ACCESSIONS S28565; S31423  
REFERENCE S28565  
#authors Carbelli, M.; Sessa, G.; Balma, S.; Morelli, G.; Rubertl, I.  
#journal Plant J. (1993) 4:469-479  
#title The Arabidopsis Athb-2 and -4 genes are strongly induced by far-red-rich light.  
#cross-references MIMD:94035194  
#accession S28565  
##molecule\_type mRNA  
##residues 1-45 ##label CAR1  
#accession S31423  
##molecule\_type DNA  
##residues 1-45 #label CAR2  
#cross-references EMBL:X68145; NID:G16178; PID:G16179  
SUMMARY ##cross-references EMBL:G68146; NID:G16330; PID:G16331  
Query Match 100.0%; Score 28; DB 2; Length 45;  
Best local similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 8 LSASL 12  
QY 31 LSASL 35

RESULT 2  
ENTRY S38564 #type fragment  
TITLE Ig kappa chain V region (ASWU1) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Mar-1998  
ACCESSIONS S38564  
REFERENCE S38559  
#authors Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.  
#submission submitted to the EMBL Data Library, September 1993  
#description Molecular analysis of mercury-induced anti-nuclear antibodies in H-2s Mice.

#accession S38564  
#status Preliminary  
#molecule-type mRNA  
#residues 1-93 #label MON  
#cross-references EMBL:X75105; NID:9414153; PID:9414154  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
SUMMARY #length 93 #checksum 1511

Query Match 100.0%; Score 28; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15  
|||  
OY 31 LSASL 35

SULT 3  
ENTRY S50530 #type complete  
TITLE hypothetical protein YEL059w - yeast (Saccharomyces cerevisiae)  
ORGANISM #formal\_name Saccharomyces cerevisiae  
DATE 28-May-1993 #sequence\_revision 24-Feb-1995 #text\_change 21-Nov-1997  
ACCESSIONS S50530  
REFERENCE S50428  
#authors Dietrich, F.S.  
#sublation Submitted to the EMBL Data Library, December 1994  
#description The sequence of S. cerevisiae cosmid 9669, 8334, 8199, and lambda clone 1160.  
#accession S50530  
#molecule-type DNA  
#residues 1-102 #label DIE  
#cross-references EMBL:U18795; NID:9603241; PID:9603259; MIPS:YEL059w  
GENETICS  
SUMMARY #map\_position 5L  
#length 102 #molecular-weight 11341 #checksum 6268

Query Match 100.0%; Score 28; DB 2; Length 102;  
Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 LSASL 74  
|||  
OY 31 LSASL 35

SULT 4  
ENTRY C33936 #type fragment  
TITLE Ig kappa chain V region (VH113) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 08-Sep-1997  
ACCESSIONS C33936  
REFERENCE A33936  
#authors Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:4664-4668  
#title Nucleotide changes in sequential variants of influenza virus hemagglutinin genes and molecular structures of corresponding monoclonal antibodies specific for each variant.  
#cross-references MUID:89282831  
#accession C33936  
#status Preliminary  
#molecule-type mRNA  
#residues 1-106 #label MEE  
#cross-references GB:J04577; NID:9623187; PID:9623189  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotrimer; immunoglobulin  
SUMMARY #length 106 #checksum 2278

Query Match 100.0%; Score 28; DB 2; Length 106;

Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15  
|||  
OY 31 LSASL 35

RESULT 5  
ENTRY PL0259 #type fragment  
TITLE Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
ACCESSIONS PL0259  
REFERENCE PL0231  
#authors Shlomchik, M.; Mascello, M.; Shan, H.; Radic, M.Z.; Pletscky, D.; Marshak-Rothstein, A.; Weigert, M.  
#journal J. Exp. Med. (1990) 171:265-297  
#title Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.  
#cross-references MUID:90111618  
#accession PL0260  
#molecule-type mRNA  
#residues 1-106 #label SHL  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotrimer; immunoglobulin  
FEATURE 1-23  
24-34 #region framework 1\  
35-49 #region complementarity-determining 1\  
50-56 #region framework 2\  
57-88 #region complementarity-determining 2\  
89-97 #region framework 3\  
98-106 #region complementarity-determining 3\  
#region framework 4

Query Match 100.0%; Score 28; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15  
|||  
OY 31 LSASL 35

RESULT 6  
ENTRY PL0260 #type fragment  
TITLE Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
ACCESSIONS PL0260  
REFERENCE PL0231  
#authors Shlomchik, M.; Mascello, M.; Shan, H.; Radic, M.Z.; Pletscky, D.; Marshak-Rothstein, A.; Weigert, M.  
#journal J. Exp. Med. (1990) 171:265-297  
#title Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.  
#cross-references MUID:90111618  
#accession PL0260  
#molecule-type mRNA  
#residues 1-106 #label SHL  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotrimer; immunoglobulin  
FEATURE 1-23  
24-34 #region framework 1\  
35-49 #region complementarity-determining 1\  
50-56 #region framework 2\  
57-88 #region complementarity-determining 2\  
89-97 #region framework 3\  
98-106 #region complementarity-determining 3\  
#region framework 4

SUMMARY #length 106 #checksum 2157

Query Match 100.0%; Score 28; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15  
|||||

QY 31 LSASL 35

RESULT 7

ENTRY B47271 #type fragment  
TITLE nitrophenyl phosphonate-specific antibody 4867 light chain VJ  
ORGANISM #formal\_name synthetic  
#note Mus musculus (house mouse) gene engineered and expressed in Escherichia coli  
#title 21-Sep-1993 #sequence\_revision 11-Aug-1995 #text\_change 11-Aug-1995

ACCESSIONS B47271  
REFERENCE A47271  
#authors Lesley, S.A.; Patten, P.A.; Schultz, P.G.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1160-1165  
#title A genetic approach to the generation of antibodies with enhanced catalytic activities.  
#cross-references M01D:93165660  
#accession B47271  
#molecule\_type DNA; protein  
#residues 1-108 #label LES  
#note sequence extracted from NCBI backbone (NCBIN:124856, NCBI:124859)  
#note parts of this sequence were determined by protein sequencing

FEATURE 24-89  
SUMMARY #disulfide\_bonds #status predicted  
#length 108 #checksum 9036

Query Match 100.0%; Score 28; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 LSASL 16  
|||||

QY 31 LSASL 35

SULT 8  
ENTRY C26405 #type complete  
TITLE Ig kappa chain V region (3D10) - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 16-Aug-1996

ACCESSIONS C26405  
REFERENCE A90518  
#authors Smith, J.A.; Margolies, M.N.  
#journal Biochemistry (1987) 26:604-612  
#title Complete amino acid sequences of the heavy and light chain variable regions from two A/J mouse antigen nonbinding monoclonal antibodies bearing the predominant p-azophenyl arsonate idio type.

#cross-references M01D:87157677  
#accession C26405  
#molecule\_type protein  
#residues 1-108 #label SMI  
#note #experimental\_source strain A/J  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SUMMARY #length 108 #molecular-weight 11944 #checksum 1684

Query Match 100.0%; Score 28; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15  
|||||

QY 31 LSASL 35

RESULT 9

ENTRY B26405 #type complete  
TITLE Ig kappa chain V region (1F6) - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 16-Aug-1996

ACCESSIONS B26405  
REFERENCE A90518  
#authors Smith, J.A.; Margolies, M.N.  
#journal Biochemistry (1987) 26:604-612  
#title Complete amino acid sequences of the heavy and light chain variable regions from two A/J mouse antigen nonbinding monoclonal antibodies bearing the predominant p-azophenyl arsonate idio type.

#cross-references M01D:87157677  
#accession B26405  
#molecule\_type protein  
#residues 1-108 #label SMI  
#note #experimental\_source strain A/J  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SUMMARY #length 108 #molecular-weight 11985 #checksum 1541

Query Match 100.0%; Score 28; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15  
|||||

QY 31 LSASL 35

RESULT 10

ENTRY KWMS09 #type complete  
TITLE Ig kappa chain V region (E109) - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996

ACCESSIONS B92808  
REFERENCE A92808  
#authors Vrana, M.; Rudikoff, S.; Potter, M.  
#journal J. Immunol. (1979) 122:1905-1910  
#title The structural basis of a hapten-inhibitable kappa-chain idio type.

#cross-references M01D:79195288  
#accession B92808  
#molecule\_type protein  
#residues 1-108 #label VRA  
COMMENT This chain was isolated from a myeloma protein that binds inulin. An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

#superfamily immunoglobulin V region; immunoglobulin homology  
heterotetramer; immunoglobulin

CLASSIFICATION  
KEYWORDS  
FEATURE 23-88  
SUMMARY #disulfide\_bonds #status predicted  
#length 108 #molecular-weight 11876 #checksum 6583

Query Match 100.0%; Score 28; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15  
|||||

QY 31 LSASL 35

RESULT 11  
ENTRY KVM682 #type complete  
TITLE Ig kappa chain V region (W3082) - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996

ACCESSIONS  
REFERENCE B92811; A01929  
#authors Johnson, N.; Stankard, J.; Paul, L.; Hood, L.  
#journal J. Immunol. (1982) 128:302-307  
#title The complete V domain amino acid sequences of two myeloma  
#cross-references MUID:82099361  
#accession B92811

COMMENT ##residues 1-108 #label JOH  
##molecule\_type protein  
##complex This chain was isolated from a myeloma protein that binds inulin.  
An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

CLASSIFICATION  
KEYWORDS #superfamily immunoglobulin V region; immunoglobulin homology  
FEATURE heterotetramer; immunoglobulin

SUMMARY  
#disulfide\_bonds #status predicted  
#length 108 #molecular\_weight 11850 #checksum 6696

Query Match 100.0%; Score 28; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15  
QY 31 LSASL 35

RESULT 12  
ENTRY S03521 #type fragment  
TITLE Ig kappa chain precursor V region (hybridoma PRF-02) - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
#journal 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 08-Sep-1997  
#accession S03521; S05066  
#cross-references EMBL:X07963; NID:933645; PID:933646

GENETICS  
#authors Adzhahov, V.A.; Stepchenko, A.G.; Deev, S.A.; Polyakovskii, O.L.  
#journal Mol. Biol. (1987) 21:945-948  
#title Structure of the variable gene coding for chi-chains of antibodies produced by hybridoma PTF-02.  
#accession S03521  
#molecule\_type DNA  
#residues 1-124 #label ADZ  
#cross-references EMBL:X07963; NID:933645; PID:933646

CLASSIFICATION  
KEYWORDS #superfamily immunoglobulin V region; immunoglobulin homology  
FEATURE heterotetramer; immunoglobulin

SUMMARY  
#domain signal sequence #status predicted #label SIG\  
#product Ig kappa chain V region #status predicted  
#label M41  
#domain V segment #label VSF\  
#domain J segment #label JSF\  
#disulfide\_bonds #status predicted  
#length 124 #checksum 9886

Query Match 100.0%; Score 28; DB 2; Length 124;

Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 28 LSASL 32  
QY 31 LSASL 35

RESULT 13  
ENTRY KVM64 #type complete  
TITLE Ig kappa chain precursor V region (MOPC 41) - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 16-Aug-1996

ACCESSIONS  
REFERENCE A93211; B93211; A93815; A94239; A01922; A01923  
#authors Seidman, J.G.; Max, E.E.; Leder, P.  
#journal Nature (1979) 280:370-375  
#title A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.  
#cross-references MUID:79221900  
#accession A93211  
##molecule\_type DNA  
##residues 1-130 #label PC41  
#accession B93211  
##molecule\_type DNA  
##residues 1-117 #label VK41  
##note the sequences were determined from the differentiated gene MOPC 41 and the germline gene VK41

REFERENCE  
#authors Burstein, Y.; Schechter, I.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720  
#title Amino acid sequence of the NH-2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda-I-type and kappa-type light chains.  
#cross-references MUID:77148916  
#accession A93815  
##molecule\_type protein  
##residues 1-33 #label BUR  
##note Met-3 is apparently used as an alternative initiator in 25% of the chains

REFERENCE  
#authors Gray, W.R.; Dreyer, W.J.; Hood, L.  
#journal Science (1967) 155:465-467  
#title Mechanism of antibody synthesis: size differences between mouse kappa chains.  
#cross-references MUID:67056897  
#accession A94239  
##molecule\_type protein  
##residues 23-49, 'B', '51-53, 'LSB', '57-58, 'Z2', '61-62, 'Bz', '65-76, 'B', '78-108, '110-130 #label GFA  
#cross-references EMBL:J01000; NID:933645; PID:933646

GENETICS  
#authors 19/1  
#journal An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.  
#superfamily immunoglobulin V region; immunoglobulin homology  
#alternative initiators; heterotetramer; immunoglobulin

CLASSIFICATION  
KEYWORDS #domain signal sequence #status experimental #label SIG1  
#product Ig kappa chain V region (MOPC 41) #status experimental #label M41  
#domain immunoglobulin homology #label IMM\  
#disulfide\_bonds #status predicted  
#length 130 #molecular\_weight 14311 #checksum 6707

SUMMARY

Query Match 100.0%; Score 28; DB 1; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 33 LSASL 37  
 11111  
 0Y 31 LSASL 35

RESULT 14  
 ENTRY B69465 #type complete  
 TITLE transcription regulator Asnc family homolog - Archaeoglobus  
 fulgidus

ORGANISM #formal\_name Archaeoglobus fulgidus  
 DATE 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change  
 02-Jul-1998

ACCESSIONS B69465  
 REFERENCE A69250  
 #authors Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson,  
 K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.;  
 Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham,  
 D.E.; Kyrpides, N.C.; Fleischmann, R.D.; Quackenbush, J.;  
 Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;  
 Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.;  
 Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.;  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman,  
 J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs,  
 T.; Artlich, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.;  
 D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.;  
 Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese,  
 C.R.; Venter, J.C.

#journal Nature (1997) 390:364-370  
 #title The complete genome sequence of the hyperthermophilic,  
 sulfate-reducing archaeon Archaeoglobus fulgidus.  
 #cross-references MUID:98049343  
 #accession B69465  
 #status preliminary; nucleic acid sequence not shown;  
 translation not shown

#molecule\_type DNA  
 #residues 1-138 #label KLE  
 #cross-references GB:AE000984; GB:AE000782; NID:92689307; PID:92648831;  
 TIGR:AF1723

SUMMARY #length 138 #molecular\_weight 15577 #checksum 3741

Query Match 100.0%; Score 28; DB 2; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 LSASL 65  
 11111  
 0Y 31 LSASL 35

RESULT 15  
 ENTRY JE0065 #type fragment  
 TITLE retroviral proteinase-like protein - human (fragment)  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change  
 24-Feb-1995

ACCESSIONS JE0065  
 REFERENCE JE0065  
 #authors Johansen, T.; Holm, T.; Bjorkild, E.  
 #journal Gene (1989) 79:259-267  
 #title Members of the RVL-H family of human endogenous  
 retrovirus-like elements are expressed in placenta.  
 #cross-references MUID:90006755

#accession JE0065  
 #molecule\_type mRNA  
 #residues 1-165 #label JOH  
 #experimental\_source placenta  
 #note readthrough of the terminator TGA may occur between the  
 codons GAR for 19-Asp and CGC for 20-Arg

SUMMARY #length 165 #checksum 5256

Query Match 100.0%; Score 28; DB 2; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 6.56e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 122 LSASL 126  
 11111  
 0Y 31 LSASL 35

Search completed: Tue Apr 20 13:56:36 1999  
 Job time : 17 secs.

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Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
n on: Tue Apr 20 13:54:52 1999; Maspar time 2.29 Seconds  
Tabular output not generated. 58.693 Million cell updates/sec

Title: >US-08-836-455-2  
Description: (31-35) from US08836455.pep (1 of 3)

Perfect Score: 28  
Sequence: 1 LSASL 5

Scoring table: PAM 150  
Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot35  
1:swissprot

Statistics: Mean 17.476; Variance 12.170; scale 1.436

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

result	No.	Score	Query Match	length	ID	Description	Pred. No.
1	28	100.0	102	1	YEG9_YEAST	HYPOTHETICAL 11.3 KD P	3.19e+02
2	28	100.0	108	1	KV5U_MOUSE	IG KAPPA CHAIN V-V REG	3.19e+02
3	28	100.0	108	1	KV5T_MOUSE	IG KAPPA CHAIN V-V REG	3.19e+02
4	28	100.0	108	1	KV5R_MOUSE	IG KAPPA CHAIN V-V REG	3.19e+02
5	28	100.0	125	1	MFAP_SACKL	MATING FACTOR ALPHA PR	3.19e+02
6	28	100.0	180	1	YFKK_BRAJA	HYPOTHETICAL PROTEIN I	3.19e+02
7	28	100.0	255	1	YFCA_HAEIN	HYPOTHETICAL PROTEIN H	3.19e+02
8	28	100.0	303	1	ARAL_STRAT	PUTATIVE ARAC-LIKE TRA	3.19e+02
9	28	100.0	304	1	ARAL_STRAT	PUTATIVE ARAC-LIKE TRA	3.19e+02
10	28	100.0	317	1	Y8F_YEAST	HYPOTHETICAL 35.4 KD P	3.19e+02
11	28	100.0	365	1	MEPB_HUMAN	MYOCYTE-SPECIFIC ENHAN	3.19e+02
12	28	100.0	367	1	YMCB_BPE41	HYPOTHETICAL PROTEIN I	3.19e+02
13	28	100.0	371	1	LEB3_SCHPO	3-ISOPROPYLMALATE DEH	3.19e+02
14	28	100.0	416	1	MYC_AVI0K	MYC TRANSFORMING PROTE	3.19e+02
15	28	100.0	416	1	MYC_CHICK	MYC TRANSFORMING PROTE	3.19e+02
16	28	100.0	417	1	YTER_ECOLI	HYPOTHETICAL ABC TRANS	3.19e+02
17	28	100.0	417	1	YGA4_YEAST	HYPOTHETICAL 46.4 KD T	3.19e+02
18	28	100.0	421	1	MYC_AVI02	MYC TRANSFORMING PROTE	3.19e+02
19	28	100.0	422	1	MYC_AVI02	MYC TRANSFORMING PROTE	3.19e+02
20	28	100.0	422	1	MYC_AVI02	MYC TRANSFORMING PROTE	3.19e+02
21	28	100.0	443	1	PORD_PSEAE	PORDIN D PRECURSOR (OOR	3.19e+02
22	28	100.0	458	1	NUAM_PETMA	NADH-UBIQUINONE OXIDOR	3.19e+02
23	28	100.0	479	1	6PGD_TRYBB	6-PHOSPHOGLUCONATE DEH	3.19e+02

24	28	100.0	489	1	TCPC_VIBCH	TOXIN CORRELATED PIL	3.19e+02
25	28	100.0	518	1	YX23_CAEEL	HYPOTHETICAL 59.7 KD P	3.19e+02
26	28	100.0	529	1	2ACB_HUMAN	PROTEIN PHOSPHATASE PP	3.19e+02
27	28	100.0	533	1	CAG2_MOUSE	BETA-1.4 N-ACETYLGLAC	3.19e+02
28	28	100.0	648	1	VEL_PCPV1	REPLICATION PROTEIN EI	3.19e+02
29	28	100.0	680	1	NOLO_HRISN	NUBULATION PROTEIN IOL	3.19e+02
30	28	100.0	709	1	TOP1_MYCCE	DNA TOPOISOMERASE I (E	3.19e+02
31	28	100.0	725	1	AREA_PENCH	NITROGEN REGULATORY PR	3.19e+02
32	28	100.0	827	1	MOF_DROME	MALES-ABSENT ON THE FI	3.19e+02
33	28	100.0	842	1	AMPN_LACDL	AMINOPEPTIDASE N (EC 3	3.19e+02
34	28	100.0	860	1	AREA_PENRO	NITROGEN REGULATORY PR	3.19e+02
35	28	100.0	865	1	NREFA_PENUR	NITROGEN REGULATORY PR	3.19e+02
36	28	100.0	870	1	YS05_CAEEL	HYPOTHETICAL 98.0 KD P	3.19e+02
37	28	100.0	876	1	AREA_EMEI1	NITROGEN REGULATORY PR	3.19e+02
38	28	100.0	882	1	AREA_ASPNG	NITROGEN REGULATORY PR	3.19e+02
39	28	100.0	925	1	PMP2_CAEEL	PERIODIC TRYPTOPHAN PR	3.19e+02
40	28	100.0	1010	1	PUR2_MOUSE	PHOSPHORIBOSYLAMINE--G	3.19e+02
41	28	100.0	1035	1	ATHA_HUMAN	POTASSIUM-TRANSPORTING	3.19e+02
42	28	100.0	1048	1	NMD5_YEAST	NONSENSE-MEDIATED RNA	3.19e+02
43	28	100.0	1150	1	2ACA_HUMAN	PROTEIN PHOSPHATASE PP	3.19e+02
44	28	100.0	1195	1	YK76_YEAST	HYPOTHETICAL 137.5 KD	3.19e+02
45	28	100.0	1472	1	A2MG_RAT	ALPHA-2-MACROGLOBULIN	3.19e+02

## ALIGNMENTS

RESULT	1	STANDARD	PRT	102 AA.
ID	YEG9_YEAST			
AC	P39982;			
DT	01-FEB-1995 (REL. 31, CREATED)			
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	HYPOTHETICAL 11.3 KD PROTEIN IN SOM1-PCMI INTERGENIC REGION.			
GN	YEO039W.			
OS	SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).			
OC	EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RA	STRAIN-S288C / AB972;			
RA	DITRICH F.S., MOLLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R.,			
RA	AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M.,			
RA	CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., HUNNICK-SMITH S.,			
RA	HYANG R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D.,			
RA	MOSEDALE D., NAKAHARA K., NAWATH A., NONGREN R., OEFNER P., OH C.,			
RA	PEREL F.X., ROBERTS D., SEHL P., SCHRAM S., SHOGEN T., SMITH V.,			
RA	TAYLOR P., WEI Y., YELTON M., BOTSTEIN D., DAVIS R.W.;			
RL	SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL; U18795; G603259; "			
KW	HYPOTHETICAL PROTEIN; TRANSMEMBRANE.			
FT	TRANSMEM 18 38			
FT	POTENTIAL.			
FT	TRANSMEM 70 90			
FT	POTENTIAL.			
FT	SEQUENCE 102 AA; 11341 MW; 5AB0614B CRC32;			
SO	SEQUENCE			
Query Match	100.0%; Score 28; DB 1; Length 102;			
Best Local Similarity	100.0%; Pred. No. 3.19e+02;			
Matches	5; Conservative			
	0; Mismatches			
	0; Indels			
	0; Gaps			
	0;			
Db	70 LSASL 74			
Oy	31 LSASL 35			
RESULT	2	STANDARD	PRT	108 AA.
ID	KV5U_MOUSE			
AC	P04946;			
DT	13-AUG-1987 (REL. 05, CREATED)			
DT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)			
DT	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN V-V REGION (NOS-89.4).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			

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RP SEQUENCE FROM N.A.
RX MEDLINE: 83271467.
RA KARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;
RL NATURE 304:320-324(1983).
CC -1- ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
DR EMBL: K00745; G196455; -.
HSSP: P01607; 1PA1.
KM IMMUNOGLOBULIN V REGION; HYBRIDOMA.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 FRAMEWORK 3.
FT DOMAIN 6 88 FRAMEWORK 4.
FT DISULFID 98 107 COMPLEMENTARITY-DETERMINING 3.
FT NON_TER 23 88 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11866 MW; D396F142 CRC32;

Query Match
Best Local Similarity 100.0%; Score 28; DB 1; Length 108;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15
OY 31 LSASL 35

RESULT 3
ID KVT_MOUSE STANDARD; PRT: 108 AA.
AC P01653;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (W3082).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82099361.
RA JOHNSON N., SLANKARD J., PAUL L., HOOD L.;
RL J. IMMUNOL. 128:302-307(1982).
CC -1- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND
BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR: B92811; KVM52.
HSSP: P01607; 1FVJ.
KM IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 FRAMEWORK 3.
FT DOMAIN 6 88 FRAMEWORK 4.
FT DISULFID 98 107 COMPLEMENTARITY-DETERMINING 3.
FT NON_TER 23 88 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11860 MW; 6CA5FA40 CRC32;

Query Match
Best Local Similarity 100.0%; Score 28; DB 1; Length 108;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15
OY 31 LSASL 35

RESULT 4
ID KVS_MOUSE STANDARD; PRT: 108 AA.
AC P01651;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

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DE 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (EPC 109).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE: 79195288.
RA VRANA M., RUDIKOFF S., POTTER M.;
RL J. IMMUNOL. 122:1905-1910(1979).
CC -1- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND
BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR: B92808; KVM509.
HSSP: P01607; 1FVJ.
KM IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 FRAMEWORK 3.
FT DOMAIN 6 88 FRAMEWORK 4.
FT DISULFID 98 107 COMPLEMENTARITY-DETERMINING 3.
FT NON_TER 23 88 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11876 MW; 3B5013E3 CRC32;

Query Match
Best Local Similarity 100.0%; Score 28; DB 1; Length 108;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15
OY 31 LSASL 35

RESULT 5
ID MFAP_SACRL STANDARD; PRT: 125 AA.
AC P06648;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE MATING FACTOR ALPHA PRECURSOR (ALPHA MATING PHEROMONE).
OS SACCAROMYCES KLUYVERI (YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IFO 1894.
RX MEDLINE: 8731894.
RA EGEL-WITANT M., HANSEN M.T.;
RL NUCLEIC ACIDS RES. 15:6303-6303(1987).
DR EMBL: Y00385; G4859.
PIR: A29120; A29120.
KM PHEROMONE; GLYCOPROTEIN; SIGNAL.
FT CHAIN 1 22 ALPHA-MATING PHEROMONE.
FT PEPTIDE 92 125 MATING FACTOR ALPHA (1ST COPY).
FT PEPTIDE 113 125 MATING FACTOR ALPHA (2ND COPY).
FT CARBOHYD 57 67 POTENTIAL.
FT CARBOHYD 67 67 POTENTIAL.
SQ SEQUENCE 125 AA; 13925 MW; F12141F8 CRC32;

Query Match
Best Local Similarity 100.0%; Score 28; DB 1; Length 125;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LSASL 11
OY 31 LSASL 35

RESULT 6
ID YPKR_BRAVA STANDARD; PRT: 180 AA.
AC P29285;

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DT 01-DEC-1992 (REL. 24, CREATED)  
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)  
 DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL PROTEIN IN FIX 5' REGION (FRAGMENT).  
 OS BRADYRHIZOBIUM JAPONICUM.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;  
 OC RHIZOBIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-1105PC4.  
 RX MEDLINE; 92202135.  
 RA ANTHAMATTEN D., SCHERB B., HENNECKE H.;  
 RL J. BACTERIOL. 174:2111-2120(1992).  
 DR EMBL; M66805; G152086; -  
 DR PIR; A42371; A42371.  
 KM HYPOTHETICAL PROTEIN.  
 FT NON\_TER 1  
 SQ SEQUENCE 180 AA; 19419 MW; 30B80F6A CRC32;  
 Query Match 100.0%; Score 28; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 3.19e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 31 LSASL 35  
 QY 31 LSASL 35  
 RESULT 7  
 ID YFCA\_HAEIN STANDARD; PRT; 255 AA.  
 AC P6490;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL PROTEIN HT0198.  
 GN HT0198.  
 OS HAEMOPHILUS INFLUENZAE.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC PASTEREILLACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-RD / KW20;  
 RX MEDLINE; 95350630.  
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,  
 RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,  
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,  
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODER A., KELLEY J.M.,  
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,  
 RA UTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDE D.M., BRANDON R.C.,  
 RA FINE L.D., FITCHMAN J.L., FUHRMANN J.L., GEOCHAGEN N.S.M.,  
 RA GNMH C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,  
 RA VENTER J.C.;  
 SCIENCE 269:496-512(1995).  
 RN [2]  
 RP REVISIONS.  
 RA WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;  
 DT SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- SIMILARITY: STRONG, TO E.COLI YFCA.  
 CC -1- SIMILARITY: TO M.LEPRAE U1177B.  
 DR EMBL; U32705; G1573158; -  
 DR TIGR; H10198; -  
 KM HYPOTHETICAL PROTEIN; TRANSMEMBRANE.  
 FT TRANSSEM 7  
 FT TRANSSEM 27  
 FT TRANSSEM 48  
 FT TRANSSEM 76  
 FT TRANSSEM 96  
 FT TRANSSEM 99  
 FT TRANSSEM 132  
 FT TRANSSEM 153  
 FT TRANSSEM 191  
 FT TRANSSEM 211  
 FT TRANSSEM 235  
 FT TRANSSEM 255  
 SQ SEQUENCE 255 AA; 27608 MW; E5E7023A CRC32;

Query Match 100.0%; Score 28; DB 1; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 3.19e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 59 LSASL 63  
 QY 31 LSASL 35  
 RESULT 8  
 ID ARAL\_STRTAT STANDARD; PRT; 303 AA.  
 AC Q03320;  
 DT 01-JUN-1994 (REL. 29, CREATED)  
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE PUTATIVE ARAC-LIKE TRANSCRIPTION REGULATOR.  
 OS STREPTOMYCES ANTIBIOTICUS.  
 OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-IMRU 3720;  
 RX MEDLINE; 93194813.  
 RA YU T.-W., CHEN C.W.;  
 RL J. BACTERIOL. 175:1847-1852(1993).  
 CC -1- SIMILARITY: BELONGS TO THE ARAC/XYS FAMILY OF TRANSCRIPTIONAL  
 CC REGULATORS.  
 DR EMBL; M66551; G153392; -  
 DR PIR; B47089; B47089.  
 DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
 DR PROSITE; PS01124; HTH\_ARAC\_FAMILY\_2; 1.  
 KM TRANSCRIPTION REGULATION; DNA-BINDING.  
 FT DNA\_BIND 218  
 FT DNA\_BIND 237  
 SQ SEQUENCE 303 AA; 32309 MW; 1BE5603C CRC32;  
 Query Match 100.0%; Score 28; DB 1; Length 303;  
 Best Local Similarity 100.0%; Pred. No. 3.19e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 17 LSASL 21  
 QY 31 LSASL 35  
 RESULT 9  
 ID ARAL\_STRLI STANDARD; PRT; 304 AA.  
 AC P35319;  
 DT 01-JUN-1994 (REL. 29, CREATED)  
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE PUTATIVE ARAC-LIKE TRANSCRIPTION REGULATOR.  
 OS STREPTOMYCES LYTIDANS.  
 OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-66 / 1326; TRANSPOSON-TN4811;  
 RX MEDLINE; 93077460.  
 RA CHEN C.W., YU T.-W., CHUNG H.-M., CHOU C.-F.;  
 RL J. BACTERIOL. 174:7762-7769(1992).  
 CC -1- SIMILARITY: BELONGS TO THE ARAC/XYS FAMILY OF TRANSCRIPTIONAL  
 CC REGULATORS.  
 DR EMBL; Z11519; G581707; -  
 DR PIR; E45277; E45277.  
 DR PIR; S19843; S19843.  
 DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
 DR PROSITE; PS01124; HTH\_ARAC\_FAMILY\_2; 1.  
 KM TRANSCRIPTION REGULATION; DNA-BINDING; TRANSPOSABLE ELEMENT.  
 FT DNA\_BIND 218  
 FT DNA\_BIND 237  
 SQ SEQUENCE 304 AA; 32878 MW; 6A9C2133 CRC32;  
 Query Match 100.0%; Score 28; DB 1; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 3.19e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	17	LSASL	21
QY	31	LSASL	35

RESULT	10	
ID	YN8F_YEAST	
AC	P53727;	
	STANDARD;	PRT;
		317 AA

	Query Match	100.0%;	Score 28:	DB 1;	Length 317;
	Best Local Similarity	100.0%;	Pred. No.	3.19e+02;	
	Matches	5; Conservative	Mismatches	0;	Indels 0; Gaps 0;
Dd	254 LSASL 258				
Oy	31 LSASL 35				

CC	-1	SIMILARITY: BELONGS TO THE MEZF2 SUBFAMILY OF MADS PROTEINS.
CC	-1	SIMILARITY: CONTAINS A DOMAIN FOUND IN SRF-TYPE TRANSCRIPTION
CC		FACTORS (MADS-DOMAIN).
DR	EMBL; X68502;	G37992; -.
DR	EMBL; X63380;	G36169; -.
DR	EMBL; AC002126;	G232909; -.
DR	MIM; 600661;	
DR	PROSITE; PS00350;	MADS_BOX_1; 1.
DR	PROSITE; PS50066;	MADS_BOX_2; 1.
KM		TRANSCRIPTION REGULATION; NUCLEAR PROTEIN; DNA-BINDING; ACTIVATOR
KM		MULTIGENE FAMILY.
FT	DOMAIN	3 57 MADS.
FT	DNA_BIND	58 86 MEZF-TYPE (POTENTIAL).
FT	DOMAIN	4 31 LYS-RICH (BASIC).
SQ	SEQUENCE	365 AA; 38638 MW; 59008CB1 CRC32;

RESULT	12	STANDARD;	PRT;	367 AA.
ID	YMCP_BP641			
AC	P26812;			
DT	01-AUG-1992 (REL. 23, CREATED)			
DT	01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)			
DT	01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)			
DE	HYPOTHEETICAL PROTEIN IN MCP 3, REGION (FRAGMENT)			
DE	LACROCCUS LACTIS BACTERIOPHAGE F4-1.			
OC	VIRIDAE; NOT YET CLASSIFIED.			

ID	RESULT	13	STANDARD:	PRT:	371 AA.
AC	LEU3_SCHPO				
AC	PI8869.				
DT	01-NOV-1980	(REL. 16, CREATED)			
DT	01-NOV-1980	(REL. 16, LAST SEQUENCE UPDATE)			
DT	01-NOV-1995	(REL. 32, LAST ANNOTATION UPDATE)			
DE	3-ISOPROPYLMALATE DEHYDROGENASE	(EC 1.1.1.85)			
DE	(IMDH) (3-IPW-DH).				
GN	LEU1.				
OS	SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).				
OC	EUKARYOTA: FUNGI: ASCOMYCOTINA: HEMIASCOMYCETES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 89106270.				
RA	KIKUCHI Y., KITAZAMA Y., SHIMATAKE G., YAMAMOTO M.:				
RL	CRRR. GENET. 14:375-379(1988).				
CC	-1- CATALYTIC ACTIVITY: 3-CARBOXY-2-HYDROXY-4-METHYLPENTANATE +				
CC	NAD(+) = 3-CARBOXY-4-METHYL-2-OXOPENTANATE + NADH (THE PRODUCT				
CC	DECARBOXYLATES TO 4-METHYL-2-OXOPENTANATE).				

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CC -1- PATHWAY: THIRD STEP IN LEUCINE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOSOL.
CC -1- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLATE
CC DEHYDROGENASES FAMILY.
DR EMBL: M36910; G173412; -.
DR HSSP: P00351; IHEX.
DR PROSITE: PS00470; IDH_LMDH; 1.
KM OXIDOREDUCTASE: LEUCINE BIOSYNTHESIS; NAD.
SQ SEQUENCE 371 AA: 39732 MW: DAEF72EA CRC32:

Query Match 100.0%; Score 28; DB 1; Length 371;
Best Local Similarity 100.0%; Pred. No. 3.19e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 308 LSASL 312
|11111
QY 31 LSASL 35

SULT 14
ID MYC_AVIOR STANDARD; PRT; 416 AA.
AC P12523;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE MYC TRANSFORMING PROTEIN.
GN V-MYC.
OS AVIAN RETROVIRUS OK10.
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC ONCOVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85190568.
RA HAYFLICK J., SEEBURG P.H., OHLSSON R., PEIFFER-OHLSSON S.,
RA WATSON D., PAPAS T., DUESBERG P.H.;
RL PROC. NATL. ACAD. SCI. U.S.A. 82:2718-2722(1985).
CC -1- THIS PROTEIN IS SYNTHESIZED AS A GAG-MYC POLYPEPTIDE.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE MYC FAMILY OF HELIX-LOOP-HELIX
CC TRANSCRIPTION FACTORS.
DR EMBL: M11352; G209657; -.
DR PIR: A22669; TVFVAC.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; 1.
KM TRANSFORMING PROTEIN: NUCLEAR PROTEIN: DNA-BINDING; ONCOGENE.
FT DNA_BIND 331 384 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
SQ SEQUENCE 416 AA: 46040 MW: 7040632F CRC32:

Query Match 100.0%; Score 28; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.19e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 LSASL 7
|11111
QY 31 LSASL 35

RESULT 15
ID MYC_CHICK STANDARD; PRT; 416 AA.
AC P01109;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE MYC PROTO-ONCOGENE PROTEIN (C-MYC).
GN MYC.
OS GALUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83169838.
RA WATSON D.K., REDDY E.P., DUESBERG P.H., PAPAS T.S.;
RL PROC. NATL. ACAD. SCI. U.S.A. 80:2146-2150(1983).
RN [2]

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RP SEQUENCE FROM N.A.
RX MEDLINE: 88302180.
RA HAHN M., HAYWARD W.;
RL MOL. CELL. BIOL. 8:2659-2662(1988).
RN [3]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE: 84272700.
RA SHIH C.-K., LINIAL M., GOODENOW M.M., HAYWARD W.S.;
RL PROC. NATL. ACAD. SCI. U.S.A. 81:4697-4701(1984).
CC -1- FUNCTION: PARTICIPATES IN THE REGULATION OF GENE TRANSCRIPTION.
CC BINDS DNA BOTH IN A NON-SPECIFIC MANNER AND ALSO SPECIFICALLY TO
CC RECOGNIZES THE CORE SEQUENCE CAG(GA)TG. SEEMS TO ACTIVATE THE
CC TRANSCRIPTION OF GROWTH-RELATED GENES.
CC -1- SUBUNIT: BINDS DNA AS AN HETERODIMER WITH MAX.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DISEASE: OVEREXPRESSION OF C-MYC IS IMPLICATED IN THE ETIOLOGY OF
CC A VARIETY OF HEMATOPOIETIC TUMORS.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE MYC FAMILY OF HELIX-LOOP-HELIX
CC TRANSCRIPTION FACTORS.
DR EMBL: J00889; G212355; -.
DR PIR: M20006; G211566; -.
DR PIR: A01352; F0CH.
DR TRANSFAC: T00181; -.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; 1.
KM PROTO-ONCOGENE; NUCLEAR PROTEIN: DNA-BINDING; PHOSPHORYLATION;
KM TRANSCRIPTION REGULATION; ACTIVATOR; GLYCOPROTEIN.
FT DOMAIN 26 30 POLY-GLU.
FT DOMAIN 163 167 POLY-PRO.
FT DOMAIN 183 186 POLY-ALA.
FT DOMAIN 398 401 POLY-ARG.
FT DNA_BIND 331 384 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT CARBOHYD 61 61 GLCNAC (BY SIMILARITY).
SQ SEQUENCE 416 AA: 46040 MW: D761BB0B CRC32:

Query Match 100.0%; Score 28; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.19e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 LSASL 7
|11111
QY 31 LSASL 35

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Search completed: Tue Apr 20 13:55:00 1999  
Job time : 8 secs.

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ot generated

1 LSASL 5

PAM 150

165420 seqs, 497

Listing first 45

sptrembl16

13:sp\_vertebrate 14:sp\_virus

Mean 16.819; Va

derived by analysis of the total score distribution

## SUMMARIES

00.0	359	2	066465
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45	28	100
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## ALIGNMENTS

**SD SEQUENCE****Matches** 5;RL SUBMITTED

DR EMBL: U57401; G2062327; -  
 RA HYPOTHETICAL PROTEIN  
 SO SEQUENCE 132 AA; 13969 MW; 525B1B91 CRC32;

Query Match 100.0%; Score 28; DB 14; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 7.03e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 17 LSASL 21  
 OY 31 LSASL 35

RESULT 3  
 ID 028551 PRELIMINARY; PRT; 138 AA.  
 AC 028551;  
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DE TRANSCRIPTIONAL REGULATORY PROTEIN, ASNC FAMILY.  
 AF1723

OS ARCHAEoglobus fulgidus.  
 OC ARCHAEABACTERIA; EURYARCHAEOTA; ARCHAEoglobales; ARCHAEoglobaceae.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;  
 RX MEDLINE; 98049343.  
 RA KLEBK H.-P., CLAYTON R.A., TOMB J.-P., WHITE O., NELSON K.E.,  
 RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,  
 RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,  
 RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., STITTON G.G., GILL S.,  
 RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,  
 RA PETERSON S., REICH C.T., MCNEIL L.R., BADGER J.H., GLODEK A., ZHOU L.,  
 RA COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,  
 RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,  
 RA NASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOISE C.R.,  
 RA VENTER J.C.;  
 RL NATURE 390:364-370(1997).  
 DR EMBL: AB000984; G2648831; -  
 DR TIGR; AF1723; -  
 KW HYPOTHETICAL PROTEIN.  
 SO SEQUENCE 138 AA; 15577 MW; 9B383364 CRC32;

Query Match 100.0%; Score 28; DB 1; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 7.03e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

61 LSASL 65  
 OY 31 LSASL 35

RESULT 4  
 ID P74274 PRELIMINARY; PRT; 154 AA.  
 AC P74274;  
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)  
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 17.5 KD PROTEIN.  
 OS SYNECHOCYSTIS SP.  
 OC EUBACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PCC6803;  
 RA TABATA S.;  
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PCC6803;  
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,  
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,  
 RA HOSOGUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NAKAO K., OKUMURA S.,

RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,  
 RA TABATA S.;  
 RL DNA RES. 3:109-136(1996).  
 DR EMBL: D90913; G1653454; -  
 KW HYPOTHETICAL PROTEIN.  
 SO SEQUENCE 154 AA; 17497 MW; 1B15C3A CRC32;

Query Match 100.0%; Score 28; DB 2; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 7.03e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 84 LSASL 88  
 OY 31 LSASL 35

RESULT 5  
 ID 015408 PRELIMINARY; PRT; 166 AA.  
 AC 015408;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE NEUTRAL PROTEINASE LARGE SUBUNIT (FRAGMENT).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PLACENTA;  
 RX MEDLINE; 90006755.  
 RA JOHANSEN T., HOLM T., BJORKLID E.,  
 RL GENE 79:259-267(1989).  
 DR EMBL: M27826; G804764; -  
 DR PRAM; PFO0077; TYP.  
 KW PROTEASE.  
 FT NON\_TER  
 SO SEQUENCE 166 AA; 17788 MW; 1DE57D18 CRC32;

Query Match 100.0%; Score 28; DB 4; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 7.03e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 123 LSASL 127  
 OY 31 LSASL 35

RESULT 6  
 ID 057725 PRELIMINARY; PRT; 182 AA.  
 AC 057725;  
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DE 182AA LONG HYPOTHETICAL PROTEIN.  
 GN PHB022.  
 OS PYROCOCUS HORIKOSHII.  
 OC ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCUS.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-013;  
 RA KANARABAYASHI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,  
 RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOTAMA A., NAGAI Y.,  
 RA SAKAI M., OGURA K., OTSUKA R., NAKAZAWA H., TAKAMITA M., OHFUKU Y.,  
 RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,  
 RA AOKI K., YOSHIZAWA T., NAKAMURA Y., MASUCHI Y., SHIZUYA H.,  
 RA KIRUCHI H.;  
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: AB009464; D1027108; -  
 SO SEQUENCE 182 AA; 19120 MW; A4F6EDEC CRC32;

Query Match 100.0%; Score 28; DB 1; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 7.03e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Db 175 LSASL 179  
 |||||  
 QY 31 LSASL 35

RESULT 7  
 ID 064015 PRELIMINARY; PRT: 204 AA.  
 AC 064015;  
 DT 01-JAN-1996 (TREMBLREL. 01, CREATED)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE LUKEMIA INHIBITORY FACTOR (LIF-LEUKEMIA INHIBITORY FACTOR).  
 GN LIF.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 SEQUENCE FROM N.A.  
 MEDLINE: 94347086.  
 HSU L.W., HEATH J.K.;  
 BIOCHEM. J. 302:103-110(1994).  
 RL EMBL: S73374; G663150; -.  
 DR MGD: MGI:96787; LIF.  
 DR PROSITE: PS00590; LIF-OSM; 1.  
 SO SEQUENCE 204 AA; 22485 MW; 8E590658 CRC32;

Query Match 100.0%; Score 28; DB 11; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 7.03e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 LSASL 118  
 |||||  
 QY 31 LSASL 35

RESULT 8  
 ID 028986 PRELIMINARY; PRT: 212 AA.  
 AC 028986;  
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DE CONSERVED HYPOTHETICAL PROTEIN.  
 GN AF1282.  
 OS ARCHAEoglobus FULCIDUS.  
 OC ARCHAEABACTERIA; EURYARCHAEOTA; ARCHAEoglobales; ARCHAEoglobaceae.  
 RN [1]  
 SEQUENCE FROM N.A.  
 STRAIN-VC-16 / DSM 4304 / ATCC 49558;  
 MEDLINE: 98049343.  
 RA KLEIN H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,  
 KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,  
 RICHARDSON D.L., KIRLAAGE A.R., GRAHAM D.E., KYRPIDES N.C.,  
 FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,  
 KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,  
 PETERSON S., REICH C.I., MCNEILL L.K., BADGER J.H., GLODOK A., ZHOU L.,  
 OVERBERGER R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,  
 COTTON M.D., SPRIGGS T., ARTACH P., KAINE B.P., STRES S.M.,  
 SADOW P.W., D'ANDREA R.P., BOWMAN C., FUJII C., GARLAND S.A.,  
 MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., MORSE C.R.,  
 RA VENTER J.C.;  
 RA NATURE 390:364-370(1997).  
 DR EMBL: AE001016; G2649299; -.  
 DR TIGR: AF1282; -.  
 KW HYPOTHETICAL PROTEIN.  
 SO SEQUENCE 212 AA; 24708 MW; C3267F18 CRC32;

Query Match 100.0%; Score 28; DB 1; Length 212;  
 Best Local Similarity 100.0%; Pred. No. 7.03e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 134 LSASL 138  
 |||||

QY 31 LSASL 35

RESULT 9  
 ID 026628 PRELIMINARY; PRT: 221 AA.  
 AC 026628;  
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 23.4 KD PROTEIN.  
 GN MTH528.  
 OS METHANOBACTERIUM THERMAUTOTROPICUM.  
 OC ARCHAEABACTERIA; EURYARCHAEOTA; METHANOBACTERIALES;  
 OC METHANOBACTERIACEAE.  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN-DELTA H;  
 RX MEDLINE: 98037514.  
 RA SMITH D.R., DOCCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,  
 RA ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,  
 RA HARRISON D., HOANG L., KENAGLE P., LUM W., POTIER B., QIU D.,  
 RA SPADFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,  
 RA JIWANI N., CARUSO A., BUSH D., SAFER H., PATWEL D., PRABHAKAR S.,  
 RA MCDONALD S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,  
 RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.,  
 RL J. BACTERIOLOGY 179:7135-7155(1997).  
 DR EMBL: AE000836; G2621602; -.  
 KW HYPOTHETICAL PROTEIN.  
 SO SEQUENCE 221 AA; 23425 MW; EF5A6F34 CRC32;

Query Match 100.0%; Score 28; DB 1; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 7.03e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 LSASL 94  
 |||||  
 QY 31 LSASL 35

RESULT 10  
 ID P97771 PRELIMINARY; PRT: 241 AA.  
 AC P97771;  
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)  
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 SEQUENCE FROM N.A.  
 RA CHUNG J.H., LEE S.D., YI K.S., SUH P.G., RYU S.H., CHOI S.J., KIM H.J.,  
 RA KIM I.J., CHOI I.H., CHUNG H.K.;  
 RA SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: U88067; G1850548; -.  
 DR PRAM: PF00047; 19.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SO SEQUENCE 241 AA; 26086 MW; EBB2D29D CRC32;

Query Match 100.0%; Score 28; DB 1; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 7.03e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 144 LSASL 148  
 |||||  
 QY 31 LSASL 35

RESULT 11  
 ID 067364 PRELIMINARY; PRT: 268 AA.  
 AC 067364;  
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)

Db	246	LSASL	250	100.0%;	Score 28;	DB 2;	Length 268;
Q7	31	LSASL	35	100.0%;	Pred. No. 7.03e+02;		
				Matches 5;	Conservative 0;	Mismatches 0;	Indels 0;
						Gaps 0;	

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RESULT      13
ID          007534
AC          007534;
DT          01-NOV-1996 (TREMBLREL. 01, CREATED)
DT          01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT          01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE          ORF YD1119C.
OS          SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
OC          EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN          [1]
RP          SEQUENCE FROM N.A.
RA          RITGER M., MUELLER-AUER S., BRUECKNER M., SCHAEFER M., WAGNER G.;
RL          SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN          [2]
RP          SEQUENCE FROM N.A.
RA          MIRS;
RL          SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC          -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC          INNER MEMBRANE (BY SIMILARITY)..
CC          -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR          EMBL: Z74167; E253042; -.
DR          PROSITE: PS00215; MITOCH_CARRIER; 2.
DR          PFMF: PFO0153; mito_carr.
KW          MITOCHONDRION; REPEAT; TRANSMEMBRANE; TRANSPORT.
SQ          SEQUENCE 307 AA; 34203 MW; CB15B354 CMC32;

Query Match      100.0%; Score 28; DB 3; Length 307;
Best Local Similarity 100.0%; Fred. No. 7.03e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0.

Db      232 LASTL 236
        |||||
Ox      31 LASTL 35

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RESULT	12	PRELIMINARY:	PRT:	266 AA.
ID	028505			
AC	028505:			
AD	01-JAN-1998	(TREMBLEL. 05, CREATED)		
DT	01-JAN-1998	(TREMBLEL. 05, LAST SEQUENCE UPDATE)		
DT	01-AUG-1998	(TREMBLEL. 07, LAST ANNOTATION UPDATE)		
DE	DIEPTIDE ABC TRANSPORTER, PERMEASE PROTEIN (DPKC).			
GN	AF1769.			
OC	ARCHAEOGLOBUS FULGIDUS.			
OS	ARCHAEAECTERIA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-VC-16 / DSM 4304 / ATCC 49558;			
	MEDLINE: 98049343.			
	KLUNK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,			
	KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,			
RA	KECHORON D.L., KERLAVAGE A.R., GRAHAM D.E., KIRPIDES N.C.,			
RA	FLEISCHMAN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,			
RA	KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,			
RA	PETERSON S., GOICH C.I., MCNELL L.R., BADGER J.H., GLODER A., ZHOU L.,			
RA	OVERBEER R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,			
RA	COTTON M.D., SPRIGGS T., ARTLACH P., KAINE B.P., SYKES S.M.,			
RA	SAWON P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,			
RA	MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOSE C.R.,			
RA	VENTER J.C.;			
RL	NATURE 390:364-370(1997).			
DR	EMBL; AE000980; G2648779; -			
DR	TIGR; AF1769; -			
KW	PFAM; pf00528; bpd_transp.			
KW	HYPOTHETICAL PROTEIN.			
CO	SEQUENCE 286 AA; 30810 MW; BE200F80 CRC32;			

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RESULT      14
ID          ID Q60458
AC          PRELIMINARY;
DT          PRT;      328 AA.
DT          01-NOV-1996 (TREMBL,REL. 01, CREATED)
DT          01-NOV-1996 (TREMBL,REL. 01, LAST SEQUENCE UPDATE)
DT          01-AUG-1998 (TREMBL,REL. 07, LAST ANNOTATION UPDATE)
DE          CATINONIC AMINO ACID TRANSPORTER-1 (FRAGMENT).
OS          CRICEULUS GASTRUS (CHINESE HAMSTER).
OC          EUDAROTA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC          EUTHERIA; RODENTIA.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE-OVARY;
RL          WANG H., KLANO E., KUHMAN S.E., KOZAK S., KAVANUGH M.P., KABAT D.;
RL          SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR          EMBL; U49797; GI469943; -.
FT          NON_TER      1
FT          NON_TER      1
SQ          SEQUENCE      328 AA;      328 MM;      0FD345C7 CRC32;

Query Match      100.0%; Score 28; DB 11; Length 328;
Best Local Similarity 100.0%; Pred. No. 7.03e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0.

Db      232 LSAST 236
      |||||
Oy      31 LSAST 35

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Query Match      100.0%: Score 28: DB 1: Length 28;
Best Local Similarity 100.0%; Pred. No. 7.03e+02;
Matches         5; Conservative 0; Mismatches 0; Gaps 0;
Db              91 LSASL 95
                11111
QY              31 LSASL 35

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RESULT	15		
ID	032253	PRELIMINARY;	PRT; 340 AA.
AC	032253;		
DT	01-JAN-1998	(TREMBL,REL. 05,	CREATED)
DT	01-JAN-1998	(TREMBL,REL. 05,	LAST SEQUENCE UPDATE)
DT	01-AUG-1998	(TREMBL,REL. 07,	LAST ANNOTATION UPDATE)
DE	YVBO PROTEIN.		
GN	YVBO.		
OS	BACILLUS SUBTILIS.		

OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.  
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-168:

RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,  
 RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,  
 RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,  
 RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,  
 RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMINGS N.J., DANIEL R.A.,  
 RA DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMERSON P.T.,  
 RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D., FRITZ C.,  
 RA FUJITA M., FUJITA Y., FUWA S., GALIZZI A., GALLERON N., GHIM S.Y.,  
 RA GLASER P., GOFPEAU A., GOLIGHTLY E.J., GRANDI G., GIUSEPPI G.,  
 RA GUY B.J., HAGA K., HALECH J., HARWOOD C.R., HENAUT A., HILBERT H.,  
 RA HOLSAPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L., JORIS B.,  
 RA KARAWATA D., KASAHARA Y., KLAEHR-BLANCARD M., KLEIN C., KOBAYASHI Y.,  
 RA KOETTER P., KONIGSTEIN G., KROCH S., KUMANO M., KURITA K., LAPIDUS A.,  
 RA LARDINOIS S., LAUBER J., LAZAREVIC V., LEE S.M., LEVINE A., LIU H.,  
 RA MASUDA S., MAUEL C., MEDIGUE C., MEDINA N., MELLAO R.P., MIZUNO M.,  
 RA MOESTL D., NAKAI S., NOBACK M., NOONE D., O'REILLY M., OGAWA K.,  
 RA OGIMARA A., OUDEGA B., PARK S.H., PARRO V., POHL T.M., PORTETELLE D.,  
 RA PORROLIK S., PRESCOTT A.M., PRESECAN E., PUJIC P., PURNELLE B.,  
 RA RAPPOPORT G., REI M., REYNOLDS S., RIEGER M., RIVOLTA C., ROCHA E.,  
 RA ROCHE B., ROSE M., SADAIE Y., SATO T., SCANLAN E., SCHLEICH S.,  
 RA SCHROETER R., SCOFONE F., SEKIGUCHI J., SEKOSKA A., SEROR S.J.,  
 RA SERROR P., SHIN B.S., SOLDI B., SOROKIN A., TACCONI E., TAKAGI T.,  
 RA TAKAHASHI H., TAKEWARI K., TAKEUCHI M., TAKAKOSHI A., TANAKA T.,  
 RA TERPSTRA P., TOGNONI A., TOSATO V., UCHIYAMA S., VANDENBOL M.,  
 RA VANNIER F., VASAROTTI A., VIARI A., WAMBUTT R., WEDLER E., WEDLER H.,  
 RA WEITENEGGER T., WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K.,  
 RA YASUMOTO K., YATA K., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E.,  
 RA YOSHIKAWA H., DANCHIN A.:  
 RL NATURE 390:249-256(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN-168:

RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.:

RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: 299121; E116083; -;  
 SO SEQUENCE 340 AA; 37382 MM; 65C3FE2D CRC32;

Query Match 100.0%; Score 28; DB 2; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 7.03e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 40 LSASL 44

31 LSASL 35

Search completed: Tue Apr 20 13:56:00 1999  
 Job time : 41 secs.

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MURINE  
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(TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Tue Apr 20 13:59:13 1999; Maspar time 2.77 Seconds  
99.212 Million cell updates/sec

Tabular output not generated.

Title: >US-08-836-455-2  
Description: (50-66) from US08836455.pep (2 of 3)  
Perfect Score: 131  
Sequence: 1 GINLHWLQOEPDGTIR 17

Scoring table: PAM 150  
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

a-geneseq32  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29

Statistics: Mean 20.705; Variance 79.996; scale 0.259

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	131	100.0	145	25	Murine monoclonal ant	3.18e-05
2	110	84.0	107	25	Murine antibody light	3.49e-03
3	110	84.0	108	4	Murine chain of M1f c1	3.49e-03
4	110	84.0	109	25	PRP 37 light chain va	3.49e-03
5	110	84.0	146	4	Sequence of the leade	1.05e-02
6	105	80.2	243	18	520C9 anti-c-erbB-2 t	1.05e-02
7	105	80.2	246	8	Sequence of 520C9 sFv	1.05e-02
8	96	73.3	534	8	Sequence of G-FIT	7.41e-02
9	94	71.8	109	18	Light chain variable	1.14e-01
10	93	71.0	90	16	Mouse derived light c	1.41e-01
11	93	71.0	107	14	Light chain variable	1.41e-01
12	93	71.0	107	14	Light chain variable	1.41e-01
13	93	71.0	107	14	Light chain variable	1.41e-01
14	93	71.0	129	24	Murine anti-human cla	1.41e-01
15	91	69.5	108	4	Murine VL kappa group	4.09e-01
16	88	67.2	109	25	PRP 28 light chain va	5.05e-01
17	87	66.4	95	25	PRP 81 light chain va	5.05e-01
18	85	64.9	124	9	Human/murine IL-1 chl	7.70e-01

19	78	59.5	109	18	R52040	Light chain variable	3.31e+00
20	78	59.5	127	6	R52670	ppM-K3 protein produc	3.31e+00
21	78	59.5	273	10	R52865	Anti-Influenza N10 sc	3.31e+00
22	77	58.8	90	16	R80079	Mouse derived light c	4.06e+00
23	76	58.0	107	6	R30768	Murine anti-CD3 Mab U	4.99e+00
24	76	58.0	108	25	W16620	Anti-human FasL antib	4.99e+00
25	76	58.0	108	21	W08834	Variable light chain	4.99e+00
26	76	58.0	108	21	W04177	Variant variable ligh	4.99e+00
27	76	58.0	109	18	R52039	Light chain variable	4.99e+00
28	76	58.0	126	2	R12237	Mouse Mab IC11 L chal	4.99e+00
29	76	58.0	127	23	W11815	Mouse anti-human Fas	4.99e+00
30	76	58.0	127	2	R12359	Light (kappa) chain v	4.99e+00
31	76	58.0	127	6	R29010	p146-K3 protein produ	4.99e+00
32	76	58.0	128	20	W06215	Mab ME4 light chain v	4.99e+00
33	76	58.0	128	5	R09426	ME4 Light Chain V Reg	4.99e+00
34	76	58.0	128	10	R53340	KM641 H chain variabl	4.99e+00
35	76	58.0	128	7	R33257	Rat immunoglobulin L	4.99e+00
36	76	58.0	131	14	R84553	MAB SCH94.03 light ch	4.99e+00
37	76	58.0	302	11	R60206	Bispecific CD3-16Fvlg	4.99e+00
38	75	57.3	107	29	W44122	Light chain variable	6.12e+00
39	73	55.7	214	6	R30776	H5216-158 murine anti	9.19e+00
40	73	55.7	214	20	W00373	Anti-CD18 chimeric an	9.19e+00
41	72	55.0	127	20	R99003	Mab VL17E6 light chal	1.12e+01
42	72	55.0	127	6	R32121	Anti-CD4 antibody MR	1.12e+01
43	71	54.2	127	8	R39265	Mouse C4G1 Ig light-c	1.38e+01
44	70	53.4	209	26	R64204	Monoclonal antibody 1	1.68e+01
45	66	50.4	108	4	R21292	Murine VL kappa group	3.72e+01

## ALIGNMENTS

RESULT	1	W27119 standard; Protein; 145 AA.
ID	W27119	
AC	04-JAN-1998	(first entry)
DT	04-JAN-1998	Murine monoclonal anti-idiotype antibody 11D10 VL region.
DE	Monoclonal antibody 11D10: anti-idiotype antibody; mucin;	
KW	human milk fat globule; HMFg; tumour; Breast cancer; vaccine.	
OS	Mus musculus.	
FM	Key	Location/Qualifiers
FT	Peptide	1..20
FT	Protein	/label- sig_peptide
FT	Region	21..145
FT	Region	/label- Mat_protein
FT	Region	21..43
FT	Region	/label- FR1
FT	Region	/note- "framework region 1"
FT	Region	44..54
FT	Region	/label- CDR1
FT	Region	/note- "complementarity determining region 1"
FT	Region	55..69
FT	Region	/label- FR2
FT	Region	/note- "framework region 2"
FT	Region	70..76
FT	Region	/label- CDR2
FT	Region	/note- "complementarity determining region 2"
FT	Region	77..108
FT	Region	/label- FR3
FT	Region	/note- "framework region 3"
FT	Region	109..117
FT	Region	/label- CDR3
FT	Region	/note- "complementarity determining region 3"
FT	Region	118..127
FT	Region	/label- FR1
FT	Region	/note- "framework region 4"
PN	W09722699-A2.	
PD	26-JUN-1997.	
PF	19-DEC-1996; U20757.	
PR	13-DEC-1996; US-575762.	
PR	20-DEC-1995; US-575762.	
PR	26-JAN-1996; US-591965.	
PA	(KENT ) UNIV KENTUCKY.	
PI	Chatterjee M, Chatterjee SK, Roan KA;	

ID	W27121 standard; Protein: 107 AA.
AC	W27121;
DT	04-JAN-1998 (first entry)
DE	Murine antibody light chain variable region consensus.
KM	Monoclonal antibody 11D10: anti-idiotypic antibody; mucin;
RW	human milk fat globule; HMEG; tumour; Breast cancer; vaccine.
OS	Mus musculus.
FH	Key
FT	Region
FT	Location/Qualifiers
FT	24..34
FT	/label= CDR1
FT	/note= "complementarity determining region 1"
FT	50..56
FT	/label= CDR2
FT	/note= "complementarity determining region 2"
FT	88..96
FT	/label= CDR3
FT	/note= "complementarity determining region 3"
FN	
PD	W09722699-A2.
FE	26-JUN-1997.
PR	19-DEC-1996; U20757.
PR	13-DEC-1996; US-575762.
PR	20-DEC-1995; US-575762.
PR	26-JAN-1996; US-591965.
PA	(KENT ) UNIV KENTUCKY.
PI	Chatterjee M. Chatterjee SK, Foon KA;
DR	WPI: 977341690/31.
PT	Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
PT	against human milk fat globule disease associated tumours,
PT	especially breast cancer
PS	Example 2; Fig 26c; 130pp: English.
CC	This polypeptide sequence comprises a consensus sequence of murine
CC	light chain variable regions (VL) selected on the basis of identity
CC	to the VL region (see W27119) of monoclonal anti-idiotypic antibody
CC	11D10. The sequences were obtained from a Genbank database
CC	search. A VH consensus (W27122) was also produced. 11D10 has at
CC	least 18 departures from the consensus sequences 7' in the light
CC	chain and 11 in the heavy chain). 8 occur within CDRs and 10
CC	outside CDRs. 11D10 polypeptides and polynucleotides can be
CC	used in vaccines and pharmaceutical compositions for the treatment
CC	of human milk fat globule-associated diseases such as breast

RESULT	3
ID	R21310 standard; Protein: 108 AA.
AC	R21310;
DT	21-MAY-1992 (first entry)
DE	Light chain of M1f clone.
KW	Fd; bacteriophage; gene III: filamentous; phagemid; capsid; coat
KW	pilus; g3p: binding; adsorption; gene VIII: diverse repertoire;
KW	specific binding pairs; replicable genetic display package.
OS	Synthetic.
PH	
FT	Key
FT	Location/Qualifiers
FT	region
FT	25..34
FT	/label= CDR1
FT	region
FT	50..56
FT	/label= CDR2
FT	region
FT	89..96
FT	/label= CDR3
NN	WO9201047-A.

PR 10-JUL-1990; GB-0134.  
PR 19-OCT-1990; GB-022845.  
PR 12-NOV-1990; GB-024503.  
PR 06-MAR-1991; GB-004744.  
PR 15-MAY-1991; GB-010549.  
PA (CABR-) CAMBRIDGE ANTIBODY.  
PI (MEDI-) MED RES COUNCIL.  
PI McCafferty J, Pope AR, Johnson KS, Hooogenboom HRJ, Griffiths AD;  
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;  
PI Winter GP, Bonnett TP;  
PT WPI: 92-056862/07.  
PR Producing members of specific binding pairs - by expression in  
PT recombinant host cells with a secreting replicable genetic  
PI display package.  
PS Example 46: Fig 52: 109pp: English.  
CC The sequence is the light chain of clone MAF encoding an scFv frag-  
CC ment specific for both hen and turkey egg lysozyme (HEL and TEL).  
CC The DNA encoding the chain was amplified from a cDNA library prep.  
CC from the spleen of an unimmunised mouse. The corresponding heavy  
CC chain was also amplified from an existing construct, pSW1-VHD1.3  
CC (Mard et al., 1989). The two fragments were assembled via a linker  
CC vector for expression on the surface of fd bacteriophage. In this  
CC way, the VL domain was replaced by a library of VL domains to allow  
CC for selection of a broader range of antibody specificities. Several  
CC clones were isolated which bound to TEL (the parent antibody D1.3  
CC binds exclusively to HEL). The sequences of the light chains of  
CC two of these clones, MFL and M21 are given in R21310 and R21311  
CC respectively. The D1.3 light chain is given in R21309.  
CC See also R21260-307, 309-312, R22450, R22565, R22567-81.  
SQ Sequence 108 AA;

Query Match 84.0%; Score 110; DB 4; Length 108;  
Best Local Similarity 82.4%; Pred. No. 3,49e-03;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps

Dd 30 gsslnvlgdeqdtlkr 46  
| :||:|||||  
Oy 50 GINLHWLQGEPODGIKTR 66

RESULT 4

ID	W18271; standard; peptide: 109 AA.
AC	W18271;
DT	09-JAN-1998 (first entry)
DE	PrP 37 light chain variable region.
KM	Pri protein (PrP; heavy chain variable region; antibody; scrapie; light chain variable region; PrP-Sc) pathogen; fatal familial insomnia;
KM	central nervous system spongiform encephalopathy; human; therapy;
KM	transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease;
KM	bovine spongiform encephalopathy; feline spongiform encephalopathy;
KM	Serstmann-Straussler-Scheinker Disease.
OS	Mus musculus.
FH	Key
FT	Region
FT	Location/Qualifiers
FT	1..23
FT	/note= "framework region 1"
FT	24..34
FT	/note= "complementarity determining region 1"
FT	35..49
FT	/note= "framework region 2"
FT	50..56
FT	/note= "complementarity determining region 2"
FT	57..68
FT	/note= "framework region 3"
FT	89..97
FT	/note= "complementarity determining region 3"
FT	98..109
FT	/note= "framework region 4"
PN	W09710505-A1.
PD	20-MAR-1997.
PF	13-SEP-1996; U14840.
PR	14-SEP-1995; US-528104.
PA	(REGC.) UNIV CALIFORNIA.
PI	Burton DR, Prusiner SB, Williamson RA;
DR	WPI: 97-202357/18.
PT	New antibodies to the scrapie isoform of prion protein - used for detection of infectious prion proteins or for treating disease such as BSE, CJD or scrapie
PS	Example 9: Fig 6, 9pp; English.
CC	W18266-W18285 represent portions of the antibodies of the invention. The antibodies of the invention are able to bind the scrapie isoform of prion central nervous system spongiform encephalopathies in humans and animals.
CC	The scrapie isoform of the prion protein (PrP-Sc) is necessary for both the transmission and pathogenesis of the transmissible neurodegenerative diseases of animals and humans. The antibodies can be used in a method of specifically bind to prion proteins associated with disease and do not bind to denatured PrP proteins not associated with disease. They can bind to prion proteins of a specific species of mammals. They can also have the ability to neutralise infectious prions. The antibodies can be used for screening for the presence of prions in products such as pharmaceuticals, food or cosmetics. They can also be used for prion neutralisation to purify products, for extraction of prion proteins or for therapy, for diseases such as bovine spongiform encephalopathy, Creutzfeldt-Jacob Disease, fatal familial insomnia or Serstmann-Straussler-Scheinker Disease, scrapie or feline spongiform encephalopathies.
CC	Sequence 109 AA:
SO	
Query Match	Score 110; DB 25; Length 109;
Best Local Similarity	82.4%; Pred. No. 3.49e-03;
Matches 14; Conservative	2; Mismatches 1; Indels 0; Gaps 0;
Dn	30 gsslnv1qpepdgtrikr 46   :   :   :   :   :   :   50 GINHLWLQOEPDGTIKR 66
Oy	
RESULT 5	
ID	P30251; standard; peptide: 146 AA.
AC	P30251;
DT	25-MAY-1992 (first entry)
DE	Sequence of the leader, variable region and first 16 AAs of the constant region of the kappa-chain (light chain) of MOpc41.

KW	Homo sapiens.
OS	Diagnostics; therapy; Immunoglobulin.
FH	Key
FT	region
FT	region
FT	region
FT	region
FT	region
FN	EP--86994-A.
PN	21-SEP-1983.
PD	10-MAR-1983; 001655.
PR	15-MAR-1982; US-358414.
PS	05-DEC-1983; US-558551.
PA	(SCHE-) SCHERING CORP.
PI	(DNAX-) DNAX RES INST.
DR	MPI; 83-772290/39.
N-PDSB:	N30165.
PT	Transformed expression vectors or plasmid(s) - with double stranded DNA sequence coding only for desired part of polypeptide chain
CC	The pref. vector or plasmid of the invention has a double-stranded DNA seq. coding for a variable region of a light or heavy chain of IgG, or for a variable region of a light or heavy chain of an immunoglobulin specific for an enzyme or surface protein. The sequence esp. codes for a variable region of a light chain having 95-115 AAs or for a variable region of a heavy chain having 110-125 AAs esp. including the D region of the heavy chain.
SQ	Sequence 146 AA;
Query Match	84.0%; Score 110; DB 4; Length 146;
Best Local Similarity	82.4%; Pred. No. 3.49e-03;
Matches 14; Conservative	2; Mismatches 1; Indels 0; Gaps 0;
Db	52 gsinlvqgpepdgtlkr 68  .:        YQ 50 GINLHWLOEPPDGTIKR 66
RESULT 6	
ID	WO2280 standard; Protein; 243 AA.
AC	WO2280;
DT	20-OCT-1996 (first entry)
DE	52OC9 anti-c-erbA-2 two single chain Fv construct.
KM	52OC9; anti-c-erbA-2 monoclonal antibody; single chain Fv; sfv;
KM	construct; polypeptide linker; C-terminal amino acid sequence;
KM	In vivo imaging; drug targeting experiment; homodimer;
KW	Increased binding avidity; tissue retention time.
OS	Homo sapiens.
FH	Key
FT	peptide
FT	location/Qualifiers
FT	118..133
FN	/label=linker
PN	US5534254-A.
PD	09-JUL-1996.
PF	06-FEB-1992; 831967.
PR	06-FEB-1992; US-831967.
PR	07-OCT-1993; US-133804.
PA	(CHIR-) CHIRON CORP.
PI	(CREA-) CREATIVE BIOMOLECULES INC.
DR	Houston IL; Huston JS; Oppermann H; Ring DB;
N-PDSB:	T36880.
PT	Compsns. contig. antigen-targeting antibody fragment constructs comprising dimec of single-chain Fv fragments
PS	Example I; Columns 33-36; 30pp; English.
CC	VARIABLE HEAVY (VH) AND VARIABLE LIGHT (VL) GENES WERE CLONED FROM AN ANTIBODY CONSTANT AND JOINING REGIONS. A TWO SINGLE CHAIN FV (SFV) GENE WAS CONSTRUCTED BY CONNECTING THE VH AND VL GENES WITH A SER-RICH POLYPEPTIDE LINKER. THE RESULTING SFV GENE,
CC	WHICH ENCODES THE PRESENT SEQUENCE, WAS INSERTED INTO AN EXPRESSION

05-FEB-1993; U01055.  
06-FEB-1992; US-831967

the human sequences and vice versa. However the residues in positions appear to be conserved

Sequence 109 AA; Protections appear to be conserved.



```

Query Match: 71.8%; Score 94; DB 18; Length 109;
Best Local Similarity 85.7%; Pred. No. 1.14e-01;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db      33 1swlqkxpdgikr 46
       | ||| | |||||
Oy      53 LHWLQOEPRDGIKR 66

RESULT 10
ID      R80078 standard; Protein; 90 AA.
AC      R80078:
DT      22-MAY-1996 (first entry)
DE      Mouse derived light chain RT3 phage antibody pattern A.
KW      Light chain; RT3; murine; catalytic antibody; bacteriophage;
        Mus musculus.
FT      Key
        Location/Qualifiers
         1..15
         /note= "framework region 1"
         16..26
         /note= "complementarity determining region 1"
         27..40
         /note= "framework region 2"
         41..47
         /note= "complementarity determining region 2"
         48..78
         /note= "framework region 3"
         79..88
         /note= "complementarity determining region 3"
         89..90
         /note= "N-terminal fragment"
         N-terminal fragment 4

FN      WO9527045-A1.
PD      12-OCT-1995.
PF      30-MAR-1994; U03420.
PR      30-MAR-1994; MO-U03420.
PA      (IGEN-) IGEN INC.
PI      Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI      Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;
PI      WPI; 95-358624/46.
DR      N-PSDB; T04625.
PT      Production of catalytic antibodies displayed on phage - by
        generating a gene library of antibody-derived domains and expressing
        it in phage vectors
PS      Disclosure: Fig 9; 13pp; English.
SC      T04625 encodes R80078 mouse derived light chain RT3 phage antibody.
CC      The DNA was used in the prepn. of catalytic antibody (CA) producing
        bacteriophage. The CAs can be used to activate/deactivate a
        biological function in an animal by enhancing the rate of cleavage,
        or formation of a specific bond within a mol. in vivo.
CC      Sequence 90 AA;

Query Match          71.0%; Score 93; DB 16; Length 90;
Best Local Similarity 76.5%; Pred. No. 1.44e-01;
Matches 13; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Db      22 gsslnvlgpe-gtkr 37
       | :|:||||| | |||
Oy      50 GINLHWLOEPRDGIKR 66

RESULT 11
ID      R79247 standard; Protein; 107 AA.
AC      R79247:
DT      21-DEC-1995 (first entry)
DE      Light chain variable region for monoclonal antibody 1F10.
KW      Monoclonal antibody; heavy metal; mercury; variable region;
        light chain.
OS      Synthetic.
PN      WO9526007-A.
PD      03-AUG-1995.
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PE 27-JAN-1995: U01199.
PR 27-JAN-1994: US-187407.
PA (BION-) BIONEERASKA INC.
PI Lopez O, Wagner FW, Wylie DE;
PR WPI: 95-275415/36.
DR N-PSDB: 097504.
PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
PS Claim 23; Page 62; 106pp; English.
CC Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate
CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC 5B6 and 3E8) were producing MAb's that were strongly positive
CC against glutathione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC by M-MLV reverse transcriptase. The primers used for cDNA synthesis
CC were complementary to the 5' end of the CH1 domain of the heavy
CC chain expressed by the hybridoma of interest, or to the 5' and of
CC the C kappa domain. Some of the primers used for cDNA synthesis are
CC shown in 097511-097518. The primer used for cDNA synthesis of the
CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region. In conjunction with
CC an appropriate V-region primer. In addition, the VH primer 097518
CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides were determined. These are given
CC in 097498-097510 and the deduced AA sequences in R79241-R79250 &
CC R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
SQ Sequence 107 AA;

Query Match 71.0%; Score 93; DB 14; Length 107;
Best Local Similarity 70.6%; Pred. No. 1,41e-01;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0

DB 30 gsslnwlgkpdqtkr 46
|:::|||||
QY 50 GINLWMLQDEPDGRTIKR 66

RESULT 12
ID R78972 standard; Protein; 107 AA.
AC R78972:
DT 21-DEC-1995 (first entry)
DE Light chain variable region for monoclonal antibody 5B6.
KW Monoclonal antibody; heavy metal; mercury; variable region;
light chain.
OS Synthetic.
PN W03520607-A.
PD 03-AUG-1995.
PF 27-JAN-1995; U01199.
PR 27-JAN-1994; US-187407.
PA (BION-) BIONEERASKA INC.
PI Lopez O, Wagner FW, Wylie DE;
PR WPI: 95-275415/36.
DR N-PSDB: 097510.
PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
PS Claim 23; Page 70; 106pp; English.
CC Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate
CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC 5B6 and 3E8) were producing MAB's that were strongly positive
CC against glutathione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with

```

CC guanidine isothiocyanate. First strand-cDNA synthesis was catalysed  
CC by MvLV reverse transcriptase. The primers used for cDNA synthesis  
CC were complementary to the 5' end of the CHI domain of the heavy  
CC chain expressed by the hybridoma of interest, or to the 5' and of  
CC the C kappa domain. Some of the primers used for cDNA synthesis are  
CC shown in 097511-097518. The primer used for cDNA synthesis of the  
CC variable region of a particular antibody polypeptide was also used  
CC for PCR amplification of that variable region, in conjunction with  
CC an appropriate V-region primer. In addition, the VH primer 097518  
CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences  
CC of the PCR amplified nucleotides were determined. These are given  
CC in 097498-097510 and the deduced AA sequences in R79241-R79250 &  
CC R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45  
CC and in the claims are different from the descriptions in the  
CC sequence listings. The descriptions in the sequence listings are  
CC used here. 107 AA;

Query Match 71.0%; Score 93; DB 14; Length 107;  
Best Local Similarity 70.6%; Pred. No. 1,41e-01;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

DB 30 gsslmwlgkpgdtkr 46  
1 : : : : :  
OY 50 GINLHMLQEPDGTIKR 66

RESULT 13  
ID R79250 standard; Protein; 107 AA.  
AC R79250;  
DT 21-DEC-1995 (first entry)  
DE Light chain variable region for monoclonal antibody 5G4.  
KW Monoclonal antibody; heavy metal; mercury; variable region;  
OS Synthetic.  
PN W05520607-A.  
PD 03-AUG-1995.  
PF 27-JAN-1995; U01199.  
PR 27-JAN-1994; US-187407.  
PA (BION-) BIONBRASKA INC.  
PI Lopez O, Wagner FW, Wylie DE;  
DR WPI: 95-273415/36.  
DR N-PSDB: 097507.

PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from  
PT monoclonal antibody(s) used for detecting, removing, adding or  
PT neutralising heavy metals  
Claim 23; Page 66; 106pp; English.  
Hybridoma antibodies have been produced with the spleen cells of  
BALB/c mouse that had received multiple injections of mercuric ions  
reacted with glutathione to produce a mercuric ion coordinate  
covalent compound which was covalently bound to keyhole limpet  
hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,  
5B6 and 3E8) were producing Mabs that were strongly positive  
against glutathione-mercuric ions but negative against glutathione  
without mercuric ions. RNA was isolated from hybridoma cells with  
guanidine isothiocyanate. The first strand cDNA synthesis was catalysed  
by MvLV reverse transcriptase. The primers used for cDNA synthesis  
were complementary to the 5' end of the CHI domain of the heavy  
chain expressed by the hybridoma of interest, or to the 5' and of  
the C kappa domain. Some of the primers used for cDNA synthesis are  
shown in 097511-097518. The primer used for cDNA synthesis of the  
variable region of a particular antibody polypeptide was also used  
for PCR amplification of that variable region, in conjunction with  
an appropriate V-region primer. In addition, the VH primer 097518  
was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences  
of the PCR amplified nucleotides were determined. These are given  
in 097498-097510 and the deduced AA sequences in R79241-R79250 &  
R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45  
and in the claims are different from the descriptions in the  
sequence listings. The descriptions in the sequence listings are  
used here. 107 AA;

CC guanidine isothiocyanate. First strand-cDNA synthesis was catalysed  
CC by MvLV reverse transcriptase. The primers used for cDNA synthesis  
CC were complementary to the 5' end of the CHI domain of the heavy  
CC chain expressed by the hybridoma of interest, or to the 5' and of  
CC the C kappa domain. Some of the primers used for cDNA synthesis are  
CC shown in 097511-097518. The primer used for cDNA synthesis of the  
CC variable region of a particular antibody polypeptide was also used  
CC for PCR amplification of that variable region, in conjunction with  
CC an appropriate V-region primer. In addition, the VH primer 097518  
CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences  
CC of the PCR amplified nucleotides were determined. These are given  
CC in 097498-097510 and the deduced AA sequences in R79241-R79250 &  
CC R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45  
CC and in the claims are different from the descriptions in the  
CC sequence listings. The descriptions in the sequence listings are  
CC used here. 107 AA;

Query Match 71.0%; Score 93; DB 14; Length 107;  
Best Local Similarity 70.6%; Pred. No. 1,41e-01;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

DB 30 gsslmwlgkpgdtkr 46  
1 : : : : :  
OY 50 GINLHMLQEPDGTIKR 66

RESULT 14  
ID W2537 standard; Protein; 129 AA.  
AC W2537;  
DT 03-NOV-1997 (first entry)  
DE Murine anti-human class II monoclonal antibody 44H104 VL chain.  
KW Antibody; light chain; variable region; hybridoma cell line 44H104;  
KW Immune response; enhance; stimulate; vaccine; immunodiagnosis;  
KW antigen delivery.  
OS Mus musculus.  
PN W09640941-A1.  
PD 19-DEC-1996.  
PF 07-JUN-1996; CA0400.  
PR 07-JUN-1995; US-483576.  
PA (CONN-) CONNAUGHT LAB LTD.  
PI Anand NN, Barber BH, Caterini JE, Cates GC, Klein MR;  
DR WPI: 97-077271/07.  
DR N-PSDB: 177851.

PT Recombinant conjugate antibody mol., modified for delivering an  
PT antigen - elicits enhanced immune response without the use of  
PT adjuvant to generate antibodies which are useful in vaccines or  
PT immuno-diagnosis  
PS Example 1; Fig 1A; 64pp; English.  
CC Novel recombinant conjugate antibody molecules comprise a monoclonal  
CC antibody specific for a surface structure of antigen presenting  
CC cells (APC), genetically modified to contain at least one antigen  
CC exclusively at one or more preselected sites. The conjugate is capable  
CC of delivering the antigen to APC and eliciting an immune response to  
CC the antigen. The new conjugates are useful as vaccines and are able  
CC to elicit an enhanced immune response without the use of an adjuvant.  
CC In a specific example, a conjugate antibody was constructed using the murine  
CC anti-human class II monoclonal antibody secreted by hybridoma  
CC 44H104. The peptide CLTB36 was chosen as antigen. It consists of  
CC a tandemly linked T and B cell epitope derived from HIV MN strain.  
CC The present sequence represents the light chain variable region  
CC from 44H104 which was used in the preparation of a conjugate with  
CC antigen CLTB36.  
Sequence 129 AA;

Query Match 71.0%; Score 93; DB 24; Length 129;  
Best Local Similarity 85.7%; Pred. No. 1,41e-01;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 55 ltwlgkpgdtkr 68  
1 : : : : :  
OY 53 LHWLQEPDGTIKR 66

RESULT 15  
ID R21286 standard; Protein; 108 AA.  
AC R21286;  
DT 21-MAY-1992 (first entry)  
DE Murine VL kappa group V chain "a", specific for phox.  
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;  
KW plus; g3p; binding; adsorption; gene VIII; diverse repertoire;  
KW specific binding pairs; replicable genetic display package.  
OS Synthetic.  
FH Key  
FT binding\_site 24..34 Location/Qualifiers  
FT binding\_site /label= CDRI  
FT binding\_site 50..56 /label= CDR1  
FT binding\_site /label= CDR2  
FT binding\_site 89..96 /label= CDR3  
FT /note= "D-X-G-X-X motif"

PN WO9201047-A.  
 PD 23-JAN-1992.  
 PF 10-JUL-1991; G01134.  
 PR 10-JUL-1990; GB-015198.  
 PR 19-OCT-1990; GB-022845.  
 PR 12-NOV-1990; GB-024503.  
 PR 06-MAR-1991; GB-004744.  
 PR 15-MAY-1991; GB-010549.  
 PA (CAMP-) CAMBRIDGE ANTIBODY.  
 PA (MED-) MED RES COUNCIL.  
 PI McCallery J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;  
 PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;  
 PI Winter GP, Bonnett TP;  
 DR WPI: 92-056862/07.  
 PT Producing members of specific binding pairs - by expression in  
 PT recombinant host cells with a secreting replicable genetic  
 PT display package.  
 PS Example 21: Fig 24: 209pp; English.  
 CC The VK sequence is one of seven (R21286-92) found to be expressed  
 CC from a single chain Fv library from an immunised mouse. The libra-  
 CC ry produces a diverse repertoire of antibody fragments specific for  
 CC 2-phenyl-3-oxazoline (phox). It was prep'd. using cDNA generated  
 CC from mRNA from mice immunised with phox coupled to chicked serum  
 CC albumin. The VH and VL kappa sequences were separately amplified  
 CC by PCR (see Q23474-84) and ligated into fdCAR2 (see Q23463) for ex-  
 CC pression on the phage surface as fusions with gene III. The result-  
 CC ing library of clones was diverse. Twenty three hapten binding  
 CC clones were sequenced revealing eight different VH genes (A-H) (see  
 CC R21264-71) in a variety of pairings with the seven different Vk  
 CC genes (a-g). Of the twenty three clones sequenced, three were of  
 CC type "a", and were "ox-like" genes. (See Berex et al, Nature 316  
 CC 412-418, 1985). They contain the DXGX motif in CDR3, the central  
 CC Gly of which is needed to create a cavity for phox. Most of the  
 CC clones were Vx-d combinations. The Kd of VH-B/Vx-d for phox-GABA  
 CC was 10 nM. Only two other combinations (of eleven tested) were  
 CC found to have higher values. This suggests that phage bearing scfv  
 CC fragments having weak affinities can be selected with antigen, pro-  
 CC bably due to the avidity of the multiple antibody heads on the  
 CC phage.  
 CC See also R21260-307, 309-311; R22450, 565-581.  
 SQ Sequence 108 AA;

Query Match 69.5%; Score 91; DB 4; Length 108;  
 Best Local Similarity 78.6%; Pred. No. 2,16e-01;  
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 33 lswlqgkpdgsikr 46  
 1 ||||| |||||  
 y 53 LHWLQOEPPDGTIKR 66

Search completed: Tue Apr 20 13:59:29 1999  
 Job time : 16 secs.

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D.: Marshak-Rothstein, A.; Weigert, M.  
J. Exp. Med. (1990) 171:265-297  
Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.  
#cross-references M01D:90111618  
#accession PLO260  
#molecule-type mRNA  
#residues 1-106 ##label SHL  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
FEATURES  
KEYWORDS  
1-23 #region framework 1\  
24-34 #region complementarity-determining 1\  
35-49 #region framework 2\  
50-56 #region complementarity-determining 2\  
57-88 #region framework 3\  
89-97 #region complementarity-determining 3\  
98-106 #region framework 4  
#length 106 #checksum 2157  
SUMMARY  
Query Match 84.0%; Score 110; DB 2; Length 106;  
Best Local Similarity 82.4%; Pred. No. 2.15e-07;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Db 30 GSSLNMLQOEPDGTIKR 46  
1-106  
OY 50 GINLHMLQOEPDGTIKR 66

ENTRY 3  
TITLE PLO259 #type fragment  
ORGANISM Ig kappa chain V region (anti-DNA, DP1VK) - mouse (fragment)  
DATE 16-Sep-1992 #sequence-revision 16-Sep-1992 #text\_change  
16-Aug-1996  
PLO259  
PLO231  
Shlomchik, M.; Masceli, M.; Shan, H.; Radic, M.Z.; Plsetsky, D.; Marshak-Rothstein, A.; Weigert, M.  
J. Exp. Med. (1990) 171:265-297  
Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.  
#cross-references M01D:90111618  
#accession PLO259  
#molecule-type mRNA  
#residues 1-106 ##label SHL  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
FEATURES  
KEYWORDS  
1-23 #region framework 1\  
24-34 #region complementarity-determining 1\  
35-49 #region framework 2\  
50-56 #region complementarity-determining 2\  
57-88 #region framework 3\  
89-97 #region complementarity-determining 3\  
98-106 #region framework 4  
#length 106 #checksum 2162  
SUMMARY  
Query Match 84.0%; Score 110; DB 2; Length 106;  
Best Local Similarity 82.4%; Pred. No. 2.15e-07;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Db 30 GSSLNMLQOEPDGTIKR 46  
1-106  
OY 50 GINLHMLQOEPDGTIKR 66

ENTRY 4  
TITLE RYMSM4 #type complete  
ORGANISM Ig kappa chain precursor V region (MOPC 41) - mouse  
CONTAINS Ig kappa chain precursor V region VK41  
#formal\_name Mus musculus #common\_name house mouse  
DATE 24-Apr-1984 #sequence-revision 24-Apr-1984 #text\_change

16-Aug-1996  
A93211; B93211; A93815; A94239; A01922; A01923  
A93211  
Seidman, J.G.; Max, E.E.; Leder, P.  
Nature (1979) 280:370-375  
A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.  
#cross-references M01D:79221900  
#accession A93211  
#molecule-type DNA  
#residues 1-130 ##label PC41  
#accession B93211  
#molecule-type DNA  
#residues 1-117 ##label VK41  
the sequences were determined from the differentiated gene MOPC 41 and the germline gene VK41  
A93815  
Burststein, Y.; Schechter, I.  
Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720  
Amino acid sequence of the NH-2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda-1-type and kappa-type light chains.  
#cross-references M01D:77148916  
#accession A93815  
#molecule-type protein  
#residues 1-33 ##label BUR  
Met-3 is apparently used as an alternative initiator in 25% of the chains  
A94239  
Gray, W.R.; Dreyer, W.J.; Hood, L.  
Science (1967) 155:465-467  
Mechanism of antibody synthesis: size differences between mouse kappa chains.  
#cross-references M01D:67056897  
#accession A94239  
#molecule-type protein  
#residues 23-49, 'B', '51-53', 'LSB', '57-58', 'Z2', '61-62', 'BZ', '65-76', 'B', '78-108', '110-130' ##label GRA  
#experimental\_source Bence Jones protein MOPC 41  
GENETICS  
#introns 19/1  
An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
FEATURES  
KEYWORDS  
1-22 #domain signal sequence #status experimental #label SIG1  
3-22 #domain signal sequence #status experimental #label SIG2  
23-130 #product Ig kappa chain V region (MOPC 41) #status experimental #label M41  
38-112 #domain immunoglobulin homology #label IMM  
45-110 #disulfide\_bonds #status predicted  
SUMMARY  
Query Match 84.0%; Score 110; DB 1; Length 130;  
Best Local Similarity 82.4%; Pred. No. 2.15e-07;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Db 52 GSSLNMLQOEPDGTIKR 68  
1-130  
OY 50 GINLHMLQOEPDGTIKR 66

ENTRY 5  
TITLE PH1062 #type fragment  
ORGANISM Ig light chain V region (clone 202.105) - mouse (fragment)  
#formal\_name Mus musculus #common\_name house mouse

```

DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
15-Jun-1996
ACCESSIONS PH1062
REFERENCE PH0971
#authors Tiliaman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
#journal J. Exp. Med. (1992) 176:761-779
#title Both IgM and IgG anti-DNA antibodies are the products of
clonally selective B cell stimulation in (NZB x NZM)F1
mice.
#accession PH1062
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-98 #label TIL
#experimental_source B cell, strain [NZB x NZM]F1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
SUMMARY #length 98 #checksum 6933

Query Match 71.8%; Score 94; DB 2; Length 98;
Best Local Similarity 85.7%; Pred. No. 1.45e-04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 33 LSWLQKRPDGIKR 46
| | | | | | | | | |
Oy 53 LHWLQEPDGIKR 66

ACCESSIONS RESULT 6
ENTRY PLO262 #type fragment
TITLE Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
ORGANISM #format_name Mus musculus #common_name house mouse
DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
16-Aug-1996
PLO262
PLO231
PLO262
PLO231
Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
D.; Marshak-Rothstein, A.; Weigert, M.
J. Exp. Med. (1990) 171:265-297
Anti-DNA antibodies from autoimmune mice arise by clonal
expansion and somatic mutation.
#cross-references MIMD:90111618
#accession PLO262
#molecule_type mRNA
#residues 1-106 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
#region framework 1\
#region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4\
SUMMARY #length 106 #checksum 658

Query Match 71.8%; Score 94; DB 2; Length 106;
Best Local Similarity 85.7%; Pred. No. 1.45e-04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 33 LSWLQKRPDGIKR 46
| | | | | | | | | |
Oy 53 LHWLQEPDGIKR 66

RESULT 7
ENTRY S17622 #type complete
TITLE Ig kappa chain V region - mouse
ORGANISM #format_name Mus musculus #common_name house mouse
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
09-May-1997
ACCESSIONS S17622
REFERENCE S17230

```

```

#authors      Jackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
#journal      Nature (1991) 352:624-628
#title        Mating antibody fragments using phage display libraries.
#cross-references MIMD:91326098
#accession    S17622
#status       preliminary
##molecule_type nucleic acid
##residues     1-91 ##label CLA
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotrimer; immunoglobulin
SUMMARY        #length 91 #molecular-weight 9895 #checksum 3446

Query Match      69.5%; Score 91; DB 2; Length 91;
Best Local Similarity 78.6%; Pred. NO. 4.70e-04;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db      25 LSWLQKPDGSIKR 38
| ||| ||| |||
QY      53 LHWLQEPDGIKR 66

RESULT      8
ENTRY       B47271      #type fragment
TITLE       nitrophenyl phosphate-specific antibody 48G7 light chain VA
ORGANISM    #formal_name synthetic
            Mus musculus (house mouse) gene engineered and expressed in
            Escherichia coli
DATE        21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change
            11-Aug-1995
ACCESSIONS  B47271
REFERENCE    A47271
            Lesley, S.A.; Patten, P.A.; Schultz, P.G.
            Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1160-1165
            A genetic approach to the generation of antibodies with
            enhanced catalytic activities.
#cross-references MIMD:9316560
#accession   B47271
            ##molecule_type DNA; protein
            ##residues     1-108 ##label IES
            #note          sequence extracted from NCBI:124856,
            NCBIR:124855)
            ##note          parts of this sequence were determined by protein
            #note          sequencing
FEATURE      #disulfide_bonds #status predicted
SUMMARY      #length 108 #checksum 9036

Query Match      69.5%; Score 91; DB 4; Length 108;
Best Local Similarity 85.7%; Pred. NO. 4.70e-04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db      34 LGWLQKPDGSIKR 47
| ||| ||| |||
QY      53 LHWLQEPDGIKR 66

RESULT      9
ENTRY       D28840      #type fragment
TITLE       Ig kappa chain V region (HP23) - mouse (fragment)
ORGANISM    #formal_name Mus musculus #common_name house mouse
DATE        29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change
            20-Mar-1998
ACCESSIONS  D28840; K25114
REFERENCE    A91028
            Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau,
            M.
            EMBO J. (1985) 4:3681-3688
            The idiotypic network and the internal image: possible
            regulation of a germ-line network by paucigene encoded Ab2
            (anti-idiotypic) antibodies in the GAT system.
#cross-references MIMD:8615012
#accession   D28840

```

```
##molecule_type mRNA
##residues 1-92 ##label OLT
##cirs--references GB:X03384; NID:g52157; PID:g52158
CLASSIFICATION ##superfamily immunoglobulin Y region; immunoglobulin homology
KEYWORDS heterodimer; immunoglobulin
SUMMARY ##length 92 ##checksum 7017
```

Query Match	68.7%;	Score 90;	DB 2;	Length 92;
Best Local Similarity	64.7%;	Pred. No. 6.95e-04;		
Matches	11;	Conservative	3;	Mismatches 3; Indels 0; Gaps 0;

```
Db      15 SVYLNMLOQKLDGTIKR 31
      ::|:||||| |||||
QY      50 GINLHMLQDEPDGTIKR 66
```

ENTRY	RESULT	10
B28840	#type fragment	
Ig kappa chain V region (HP27)	- mouse (fragment)	
#format_name Mus musculus	#common_name house mouse	
29-Aug-1987	#sequence_revision 29-Aug-1987	#text_change

ACCESSIONS	REFERENCE	authors
B28840; 125114	A91028	Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau M.

#Journal EMBO J. (1985) 4:3681-3688  
#Title The idiotypic network and the internal image: possible regulation of a germ-line network by paucigen encoded Ab2 (anti-idiotypic) antibodies in the GAT system.  
#Accession EMBL accession number: 07111

#cross\_references molu:6615612  
 #accession B28840  
 #molecule\_type mRNA  
 #residues 1-101 ##label OLT  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 KEYWORDS heterotetramer; Immunoglobulin  
 #length 101 #checksum 7015  
 SUMMARY

Query Match	64.1%;	Score 84;	DB 2;	Length 101;
Best Local Similarity	58.8%;	Pred. No. 6.97e-03;		
Matches	10;	Conservative	4;	Mismatches 3; Indels 0; Gaps 0;

```
Db      24 SVYLNLQRLDGTIKR 40
        ::|:|:|:|:|
Qy      50 GINLHMLQEPDGTIKR 66
```

LT	11	
TYPE	C28840	#type fragment
TITLE	Ig kappa chain V region (HP22)	- mouse (fragment)
ORGANISM	#formal_name Mus musculus	#common_name house mouse
DATE	29-Aug-1987	#sequence_revision 29-Aug-1987 #text_changes

ACCESSIONS	REFERENCE	#authors
C28840; J25114	A91028	Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau

#journal #title	EMBO J. (1985) 4:3681-3688
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigenic encoded Ab2 (anti-idiotypic) antibodies in the GAT system.	

```
##molecule-type mRNA
##residues 1-101 ##label OIL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
#length 101 #checksum 5983
SUMMARY
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Query Match	64.18;	Score 84;	DB 2;	Length 101;
Best Local Similarity	58.88;	Pred. No. 6.97e-03;		
Matches	10;	Conservative	4;	Mismatches 3; Indels 0; Gaps 0;

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Db      24 SVYLNWLQRLDGTIKR 40
      ::|::|::|::|
QY     50 GINLHWLQQEPDGTIKR 66

```

RESULT	12
ENTRY	S38564
TITLE	Ig kappa chain V region (ASW1) - mouse (fragment)
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Mar-1998

ACCESSIONS	
REFERENCE	
S38564	
S38559	
#authors	Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
#submission	submitted to the EMBL Data Library, September 1993
#description	Molecular analysis of mercury-induced anti-nuclear
	antibodies in H-2s Mice.

```

#accession      S38564
#status         preliminary
#molecule-type mRNA
##residues      1-93  ##label MON
##cross-references EXBLT:X75105; NID:q44153; PID:q44154
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS         immunoglobulin
#length 93      #checksum 1511
SUMMARY

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Query Match	58.0%;	Score 76;	DB 2;	Length 93;
Best Local Similarity	69.2%;	Pred. No. 1.35e-01;		
Matches	9;	Conservative	2;	Mismatches 2;
				Indels 0;
				Gaps 0;

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Db      33 LNWYQQKPPDGTVK 45
      | : | | | | : |
QY      53 LHWLQQEPDGTIK 65

```

## RESULT 13

ENTRY	PH0087	#type	fragment		
TITLE	Ig kappa chain V region (anti-cyclosporin C and D) - mouse (fragment)				
ORGANISM	#formal_name	Mus musculus	#common_name	house mouse	
DATE	15-Jan-1993	#sequence_revision	15-Jan-1993	#text_change	20-Mar-1998

**#journal** Scmlter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher,  
H.P.; Quesniaux, V.F.J.; Van Regenmortel, M.H.V.  
**#title** Mol. Immunol. (1990) 27:1029-1038  
Analysis of the structural diversity of monoclonal antibodies  
to cyclosporine.

```
#cross-references MWID:91042649
#accession PH0087
##molecule-type mRNA
##residues 1-105 ##label SCH
##cross-references GB:X57639; NID:q296839; PID:q296840
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
```

```

24-34      #region complementarity-determining 1V
50-56      #region complementarity-determining 2V
89-97      #region complementarity-determining 3
SUMMARY    #length 105 #checksum 9783

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Query Match 58.0%; Score 76; DB 2; Length 105;  
Best Local Similarity 69.28; Pred. No. 1.35e-01;  
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db      33  LNWYQQKPDGTVK 45
          | : | | | | | : |
QY      53  LHWLQEQEPDGTIK 65

```

RESULT	14	
ENTRY	A48677	#type fragment

Page 4



TITLE Ig kappa chain V-J region (48) - mouse (fragment)  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 DATE 19-May-1994 #sequence\_revision 19-May-1994 #text\_change  
 20-Mar-1998

# ACCESSIONS

## REFERENCE

## #authors

Tassignon, J.; Bratt, M.; Jamila, I.; Urbain, J.; Gottlieb,  
 P.; Brown, A.; Hasemann, C.A.; Capra, J.D.; Meek, K.  
 Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9508-9512

Molecular characterization of monoclonal CRI-A-positive  
 anti-arsenate antibodies derived from idiotype-negative  
 mice bearing a light chain polymorphism.

## #title

A48677

## #accession

preliminary; not compared with conceptual translation

## #status

A48677

## #molecule\_type

mRNA

## CLASSIFICATION

#residues 1-107 #label TAS

## KEYWORDS

#superfamily immunoglobulin V region; immunoglobulin homology

## SUMMARY

#length 107 #checksum 7886

## Query Match

Score 76; DB 2; Length 107;

## Best Local Similarity

69.2%; Pred. No. 1.35e-01;

## Matches

9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 33 LNWYQOKPDGTVK 45

OY 53 LHWLQOEPDGTIK 65

## RESULT 15

## ENTRY

## TITLE

## ORGANISM

## DATE

## ACCESSIONS

## REFERENCE

## #authors

## #journal

## #title

## #accession

## #status

## #molecule\_type

## #residues

## CLASSIFICATION

## KEYWORDS

## SUMMARY

## #length

## #checksum

## Query Match

Score 76; DB 2; Length 107;

## Best Local Similarity

69.2%; Pred. No. 1.35e-01;

## Matches

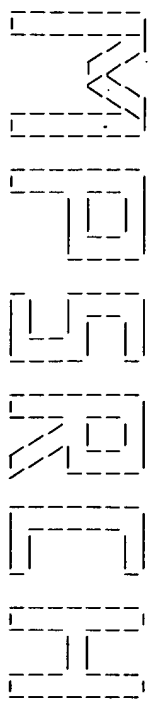
9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 33 LNWYQOKPDGTVK 45

OY 53 LHWLQOEPDGTIK 65

Search completed: Tue Apr 20 13:58:55 1999  
 Job time: 13 secs.

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(TM)

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Distribution rights by Oxford Molecular Ltd

MPearch\_pp protein - protein database search, using Smith-Waterman algorithm  
on: Tue Apr 20 14:04:22 1999; Maspar time 2.65 seconds  
67.085 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-836-455-1\_1  
Description: (24-34) from trans.pep (1 of 3)  
Perfect Score: 63  
Sequence: 1 MTQSPSSLSAS 11

Scoring table:  
PAM 150  
Gap 11

Searched: 131922 seqs, 16180660 residues  
Post-processing: Minimum Match 08  
Listing first 45 summaries

Database: a-genseq32  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29

Statistics: Mean 15.144; Variance 52.220; scale 0.290

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	63	100.0	104	29	W52225	Antibody LD2-4-VL cha 3.52e+00
2	63	100.0	105	29	W52217	Antibody LD1-84-VL ch 3.52e+00
3	63	100.0	105	29	W52239	Antibody LD1-6-17-VL 3.52e+00
4	63	100.0	105	29	W52241	Antibody LD1/2-6-3-VL 3.52e+00
5	63	100.0	105	29	W52219	Antibody LD1-110-VL c 3.52e+00
6	63	100.0	105	29	W52237	Antibody LD2-20-VL ch 3.52e+00
7	63	100.0	105	29	W52233	Antibody LD2-14-VL ch 3.52e+00
8	63	100.0	106	29	W52213	Antibody LD1-40-VL ch 3.52e+00
9	63	100.0	106	29	W52215	Antibody LD1-52-VL ch 3.52e+00
10	63	100.0	106	29	W52227	Antibody LD1-52-VL ch 3.52e+00
11	63	100.0	106	29	W52221	Antibody LD1-117-VL c 3.52e+00
12	63	100.0	106	29	W52242	Humanised alpha-4 int 3.52e+00
13	63	100.0	107	29	W41390	Humanised alpha-4 int 3.52e+00
14	63	100.0	107	29	W41397	Anti-CEA antibody 11g 3.52e+00
15	63	100.0	107	29	W23953	Chimeric humanised Mu 3.52e+00
16	63	100.0	107	29	W44123	Light chain variable 3.52e+00
17	63	100.0	107	29	W27568	Anti-TNF-alpha antibo 3.52e+00
18	63	100.0	107	21	W11920	Humanised Mab SK48-E2 3.52e+00

19	63	100.0	107	14	R79247	Light chain variable 3.52e+00
20	63	100.0	107	14	R78972	Light chain variable 3.52e+00
21	63	100.0	108	27	W23440	Modified light chain 3.52e+00
22	63	100.0	108	27	W23439	Modified light chain 3.52e+00
23	63	100.0	108	28	W23442	hm12 light chain 3.52e+00
24	63	100.0	108	21	W04177	Variant variable 11gh 3.52e+00
25	63	100.0	108	5	R28751	Light chain variable 3.52e+00
26	63	100.0	113	29	W42472	Interleukin-5 humanis 3.52e+00
27	63	100.0	117	28	W41147	Human vkap65.15 fra 3.52e+00
28	63	100.0	126	28	W36164	Humanised light chain 3.52e+00
29	63	100.0	126	14	R76678	Human/murine chimeric 3.52e+00
30	63	100.0	126	14	R76677	Human/murine chimeric 3.52e+00
31	63	100.0	126	14	R76676	Human/murine chimeric 3.52e+00
32	63	100.0	126	14	R76675	Human/murine chimeric 3.52e+00
33	63	100.0	126	14	R76680	Human/murine chimeric 3.52e+00
34	63	100.0	126	19	W04388	Chimeric human/murin 3.52e+00
35	63	100.0	128	27	W31691	Humanized anti-VLA-4 3.52e+00
36	63	100.0	128	18	R90684	Humanized 5C7.29 anti 3.52e+00
37	63	100.0	214	26	W34504	Light chain of human1 3.52e+00
38	63	100.0	214	26	W34506	Light chain of full 1 3.52e+00
39	63	100.0	224	21	W11638	Human anti-RSV monocl 3.52e+00
40	63	100.0	235	29	W41811	Humanised light chain 3.52e+00
41	63	100.0	235	29	W41398	Humanised antibody 80 3.52e+00
42	63	100.0	235	21	W11640	Human anti-RSV monocl 3.52e+00
43	63	100.0	240	29	W23954	Chimeric humanised Mu 3.52e+00
44	63	100.0	245	19	R98943	Humanised anti-CD38 m 3.52e+00
45	63	100.0	355	28	W35133	R. plapiens recombinan 3.52e+00

## ALIGNMENTS

RESULT 1  
ID W52225 standard; Protein: 104 AA.

AC W52225; 12-JUN-1998 (first entry)  
DE Antibody LD2-4-VL chain sequence.  
DT Antibody: variable heavy chain; VH chain: variable light chain; VL chain:  
KW Rhesus D antigen: anti-Rhesus D immunoglobulin; HDN: therapy.  
KW Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
OS Homo sapiens.  
PN W09749809-A1.  
PD 31-DEC-1997.  
PE 20-JUN-1997; E03253.  
PI 24-JUN-1996; BP-810421.  
PR (ROT-K) ROTKREUTSTITUNG ZENT LAB BLUTSPENDE.  
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,  
PI Vogel M;  
DR WPI: 98-077173/07.  
DR N-PSDB: V19749.  
PT New Rhesus D antigen binding polypeptide(s) - used to neutralise  
PT Rhesus D antigen in therapy, e.g. for treating idiopathic  
PT thrombocytopenic purpura  
PS Claim 1: Fig 7B; 68pp; English.  
CC This sequence is the antibody LD2-4-VL chain sequence, which is a  
CC polypeptide of the invention. The polypeptides are capable of forming  
CC antigen binding structures with specificity for Rhesus D antigens which  
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
CC variable heavy (VH) and variable light (VL) chain sequences. The  
CC antibodies are active against the Rhesus D antigen. They can be used for  
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
CC protection of Rhesus negative women before or immediately after the birth  
CC of a Rhesus positive child to prevent haemolytic disease of the newborn  
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
CC immunoglobulin can be used after transfusions of Rhesus positive blood  
CC to Rhesus negative recipients in order to prevent sensitisation to the  
CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
SQ Sequence 104 AA;

Query Match 100.0%; Score 63; DB 29; Length 104;  
Best local Similarity 100.0%; Pred. No. 3.52e+00;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 mtgspsslsas 12  
 |||||  
 OY 24 MTQSPSSLSAS 34

RESULT 2  
 ID W52217 standard; Protein: 105 AA.  
 AC W52217:  
 DT 12-JUN-1998 (first entry)  
 DE Antibody LDI-84-VL chain sequence.  
 KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;  
 KM Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
 OS Homo sapiens.  
 PN MO9749809-A1.  
 PD 31-DEC-1997.  
 PE 20-JUN-1997; E03253.  
 PR 24-JUN-1996; EP-810421.  
 PT (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.  
 PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,  
 Vogel M; 98-077173/07.  
 DR N-PSDB: V19741.  
 PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise  
 Rhesus D antigen in therapy, e.g. for treating idiopathic  
 thrombocytopenic purpura.  
 PS Claim 1, Fig 3B; 68pp; English.  
 CC This sequence is the antibody LDI-84-VL chain sequence, which is a  
 polypeptide of the invention. The polypeptides are capable of forming  
 CC antigen binding structures with specificity for Rhesus D antigens which  
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
 CC variable heavy (VH) and variable light (VL) chain sequences. The  
 CC antibodies are active against the Rhesus D antigen. They can be used for  
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
 CC protection of Rhesus negative women before or immediately after the birth  
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn  
 CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood  
 CC to Rhesus negative recipients in order to prevent sensitisation to the  
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
 SQ Sequence 105 AA.

Query Match 100.0%; Score 63; DB 29; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 mtgspsslsas 12  
 |||||  
 OY 24 MTQSPSSLSAS 34

RESULT 3  
 ID W52239 standard; Protein: 105 AA.  
 AC W52239:  
 DT 12-JUN-1998 (first entry)  
 DE Antibody LDI-6-17-VL chain sequence.  
 KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;  
 KM Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
 OS Homo sapiens.  
 PN MO9749809-A1.  
 PD 31-DEC-1997.  
 PE 20-JUN-1997; E03253.  
 PR 24-JUN-1996; EP-810421.  
 PT (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.  
 PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,  
 Vogel M; 98-077173/07.  
 DR N-PSDB: V19763.  
 PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise  
 Rhesus D antigen in therapy, e.g. for treating idiopathic  
 thrombocytopenic purpura.

PS Claim 1; Fig 14B; 68pp; English.  
 CC This sequence is the antibody LDI-6-17-VL chain sequence, which is a  
 CC polypeptide of the invention. The polypeptides are capable of forming  
 CC antigen binding structures with specificity for Rhesus D antigens which  
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
 CC variable heavy (VH) and variable light (VL) chain sequences. The  
 CC antibodies are active against the Rhesus D antigen. They can be used for  
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
 CC protection of Rhesus negative women before or immediately after the birth  
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn  
 CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood  
 CC to Rhesus negative recipients in order to prevent sensitisation to the  
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
 SQ Sequence 105 AA.

Query Match 100.0%; Score 63; DB 29; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 mtgspsslsas 12  
 |||||  
 OY 24 MTQSPSSLSAS 34

RESULT 4  
 ID W52241 standard; Protein: 105 AA.  
 AC W52241:  
 DT 12-JUN-1998 (first entry)  
 DE Antibody LDI-2-6-3-VL chain sequence.  
 KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;  
 KM Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
 OS Homo sapiens.  
 PN MO9749809-A1.  
 PD 31-DEC-1997.  
 PE 20-JUN-1997; E03253.  
 PR 24-JUN-1996; EP-810421.  
 PT (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.  
 PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,  
 Vogel M; 98-077173/07.  
 DR N-PSDB: V19765.  
 PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise  
 Rhesus D antigen in therapy, e.g. for treating idiopathic  
 thrombocytopenic purpura.  
 PS Claim 1; Fig 15B; 68pp; English.  
 CC This sequence is the antibody LDI-2-6-3-VL chain sequence, which is a  
 CC polypeptide of the invention. The polypeptides are capable of forming  
 CC antigen binding structures with specificity for Rhesus D antigens which  
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
 CC variable heavy (VH) and variable light (VL) chain sequences. The  
 CC antibodies are active against the Rhesus D antigen. They can be used for  
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
 CC protection of Rhesus negative women before or immediately after the birth  
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn  
 CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood  
 CC to Rhesus negative recipients in order to prevent sensitisation to the  
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
 SQ Sequence 105 AA.

Query Match 100.0%; Score 63; DB 29; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 mtgspsslsas 12  
 |||||  
 OY 24 MTQSPSSLSAS 34

RESULT 5  
ID W52219 standard; Protein: 105 AA.  
AC W52219;  
DE 12-JUN-1998 (first entry)  
DE Antibody LD1-110-VL chain sequence.  
KW Antibody; variable heavy chain; VH chain; variable light chain; VL chain;  
KW Rhesus D antigen; anti-rhesus D immunoglobulin; HDN; therapy;  
KW Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
OS Homo sapiens.  
PN MO9749809-A1.  
PD 31-DEC-1997.  
PF 20-JUN-1997; E03253.  
PR 24-JUN-1996; EP-810421.  
PI (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.  
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,  
PI Vogel M;  
PI WPI: 98-077173/07.  
DR N-PSDB: V19743.  
DR New Rhesus D antigen binding poly:peptide(s) - used to neutralise  
thrombocytopenic purpura  
thrombocytopenic purpura  
Claim 1: Fig 4B; 68bp; English.  
CC This sequence is the antibody LD1-110-VL chain sequence, which is a  
polypeptide of the invention. The polypeptides are capable of forming  
antigen binding structures with specificity for Rhesus D antigens which  
include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
CC variable heavy (VH) and variable light (VL) chain sequences. The  
CC antibodies are active against the Rhesus D antigen. They can be used for  
treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
CC protection of Rhesus negative women before or immediately after the birth  
of a Rhesus positive child to prevent haemolytic disease of the newborn  
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
immunoglobulin can be used after transfusions of Rhesus positive blood  
to Rhesus negative recipients in order to prevent sensitisation to the  
CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
SQ Sequence 105 AA;  
Query Match 100.0%; Score 63; DB 29; Length 105;  
Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 2 mtgspssas 12  
|||  
QY 24 MTGSPSSAS 34  
SOUT 6  
W52237 standard; Protein: 105 AA.  
DE 12-JUN-1998 (first entry)  
DE Antibody LD2-20-VL chain sequence.  
KW Antibody; variable heavy chain; VH chain; variable light chain; VL chain;  
KW Rhesus D antigen; anti-rhesus D immunoglobulin; HDN; therapy;  
KW Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
OS Homo sapiens.  
PN MO9749809-A1.  
PD 31-DEC-1997.  
PF 20-JUN-1997; E03253.  
PR 24-JUN-1996; EP-810421.  
PI (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.  
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,  
PI Vogel M;  
PI WPI: 98-077173/07.  
DR N-PSDB: V19743.  
DR New Rhesus D antigen binding poly:peptide(s) - used to neutralise  
thrombocytopenic purpura  
thrombocytopenic purpura  
Claim 1: Fig 13B; 68bp; English.  
CC This sequence is the antibody LD2-20-VL chain sequence, which is a  
polypeptide of the invention. The polypeptides are capable of forming  
antigen binding structures with specificity for Rhesus D antigens which  
include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of

CC variable heavy (VH) and variable light (VL) chain sequences. The  
CC antibodies are active against the Rhesus D antigen. They can be used for  
treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
CC protection of Rhesus negative women before or immediately after the birth  
of a Rhesus positive child to prevent haemolytic disease of the newborn  
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
immunoglobulin can be used after transfusions of Rhesus positive blood  
to Rhesus negative recipients in order to prevent sensitisation to the  
CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
SQ Sequence 105 AA;  
Query Match 100.0%; Score 63; DB 29; Length 105;  
Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 2 mtgspssas 12  
|||  
QY 24 MTGSPSSAS 34  
SOUT 7  
W52233 standard; Protein: 105 AA.  
DE 12-JUN-1998 (first entry)  
DE Antibody LD2-14-VL chain sequence.  
KW Antibody; variable heavy chain; VH chain; variable light chain; VL chain;  
KW Rhesus D antigen; anti-rhesus D immunoglobulin; HDN; therapy;  
KW Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
OS Homo sapiens.  
PN MO9749809-A1.  
PD 31-DEC-1997.  
PF 20-JUN-1997; E03253.  
PR 24-JUN-1996; EP-810421.  
PI (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.  
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,  
PI Vogel M;  
PI WPI: 98-077173/07.  
DR N-PSDB: V19743.  
DR New Rhesus D antigen binding poly:peptide(s) - used to neutralise  
thrombocytopenic purpura  
thrombocytopenic purpura  
Claim 1: Fig 11B; 68bp; English.  
CC This sequence is the antibody LD2-14-VL chain sequence, which is a  
polypeptide of the invention. The polypeptides are capable of forming  
antigen binding structures with specificity for Rhesus D antigens which  
include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
CC variable heavy (VH) and variable light (VL) chain sequences. The  
CC antibodies are active against the Rhesus D antigen. They can be used for  
treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
CC protection of Rhesus negative women before or immediately after the birth  
of a Rhesus positive child to prevent haemolytic disease of the newborn  
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
immunoglobulin can be used after transfusions of Rhesus positive blood  
to Rhesus negative recipients in order to prevent sensitisation to the  
CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
SQ Sequence 105 AA;  
Query Match 100.0%; Score 63; DB 29; Length 105;  
Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 2 mtgspssas 12  
|||  
QY 24 MTGSPSSAS 34  
SOUT 8  
W52213 standard; Protein: 106 AA.  
AC W52213;  
DE 12-JUN-1998 (first entry)  
DE Antibody LD1-40-VL chain sequence.

KM Antibody: variable heavy chain; VH chain; variable light chain; VL chain;  
KM Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;  
KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
OS Homo sapiens.  
PN MO9749809-A1.  
PD 31-DEC-1997.  
PE 20-JUN-1997; E03253.  
PR 24-JUN-1996; EP-810421.  
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.  
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,  
PI Vogel M;  
DR WPI: 98-077173/07.  
DR N-PSDB: V19737.  
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise  
PT Rhesus D antigen in therapy, e.g. for treating idiopathic  
PT thrombocytopenic purpura  
PS Claim 1; Fig 1B; 68pp; English.  
CC This sequence is the antibody LD1-40-VL chain sequence, which is a  
CC polypeptide of the invention. The polypeptides are capable of forming  
CC antigen binding structures with specificity for Rhesus D antigens which  
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
CC variable heavy (VH) and variable light (VL) chain sequences. The  
CC antibodies are active against the Rhesus D antigen. They can be used for  
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
CC protection of Rhesus positive child to prevent haemolytic disease of the newborn  
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood  
CC to Rhesus negative recipients in order to prevent sensitisation to the  
CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
SQ Sequence 106 AA;  
Query Match 100.0%; Score 63; DB 29; Length 106;  
Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 2 mtgspsslsas 12  
|||||  
OY 24 MTGSPSSLAS 34  
RESULT 9  
ID W52215 standard; Protein; 106 AA.  
AC W52215;  
DT 12-JUN-1998 (first entry)  
DE Antibody LD1-52-VL chain sequence.  
KM Antibody: variable heavy chain; VH chain; variable light chain; VL chain;  
KM Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;  
KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
OS Homo sapiens.  
PN MO9749809-A1.  
PD 31-DEC-1997.  
PE 20-JUN-1997; E03253.  
PR 24-JUN-1996; EP-810421.  
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.  
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,  
PI Vogel M;  
DR WPI: 98-077173/07.  
DR N-PSDB: V19739.  
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise  
PT Rhesus D antigen in therapy, e.g. for treating idiopathic  
PT thrombocytopenic purpura  
PS Claim 1; Fig 2B; 68pp; English.  
CC This sequence is the antibody LD1-52-VL chain sequence, which is a  
CC polypeptide of the invention. The polypeptides are capable of forming  
CC antigen binding structures with specificity for Rhesus D antigens which  
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
CC variable heavy (VH) and variable light (VL) chain sequences. The  
CC antibodies are active against the Rhesus D antigen. They can be used for  
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
CC protection of Rhesus negative women before or immediately after the birth

CC of a Rhesus positive child to prevent haemolytic disease of the newborn  
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood  
CC to Rhesus negative recipients in order to prevent sensitisation to the  
CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
SQ Sequence 106 AA;  
Query Match 100.0%; Score 63; DB 29; Length 106;  
Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 2 mtgspsslsas 12  
|||||  
OY 24 MTGSPSSLAS 34  
RESULT 10  
ID W52227 standard; Protein; 106 AA.  
AC W52227;  
DT 12-JUN-1998 (first entry)  
DE Antibody LD2-5-VL chain sequence.  
KM Antibody: variable heavy chain; VH chain; variable light chain; VL chain;  
KM Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;  
KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
OS Homo sapiens.  
PN MO9749809-A1.  
PD 31-DEC-1997.  
PE 20-JUN-1997; E03253.  
PR 24-JUN-1996; EP-810421.  
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.  
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,  
PI Vogel M;  
DR WPI: 98-077173/07.  
DR N-PSDB: V19751.  
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise  
PT Rhesus D antigen in therapy, e.g. for treating idiopathic  
PT thrombocytopenic purpura  
PS Claim 1; Fig 8B; 68pp; English.  
CC This sequence is the antibody LD2-5-VL chain sequence, which is a  
CC polypeptide of the invention. The polypeptides are capable of forming  
CC antigen binding structures with specificity for Rhesus D antigens which  
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
CC variable heavy (VH) and variable light (VL) chain sequences. The  
CC antibodies are active against the Rhesus D antigen. They can be used for  
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
CC protection of Rhesus negative women before or immediately after the birth  
CC of a Rhesus positive child to prevent haemolytic disease of the newborn  
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood  
CC to Rhesus negative recipients in order to prevent sensitisation to the  
CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
SQ Sequence 106 AA;  
Query Match 100.0%; Score 63; DB 29; Length 106;  
Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 2 mtgspsslsas 12  
|||||  
OY 24 MTGSPSSLAS 34  
RESULT 11  
ID W52221 standard; Protein; 106 AA.  
AC W52221;  
DT 12-JUN-1998 (first entry)  
DE Antibody LD1-117-VL chain sequence.  
KM Antibody: variable heavy chain; VH chain; variable light chain; VL chain;  
KM Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;  
KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
OS Homo sapiens.  
PN MO9749809-A1.

PD 31-DEC-1997. E03253.  
 PF 20-JUN-1997; EP-810421.  
 PR 24-JUN-1996; EP-810421.  
 PA (ROR-) RORKEUZSTIFTUNG ZENT LAB BLUTSPENDE.  
 PI Amstutz H, Imboden W, Miescher S, Morell A, Stadler B,  
 PI Vogel M;  
 DR WPI: 98-077173/07.  
 DR N-PSDB: V19745.  
 PR New Rhesus D antigen binding polypeptide(s) - used to neutralise  
 PR Rhesus D antigen in therapy, e.g. for treating idiopathic  
 PR thrombocytopenic purpura  
 PS Claim 1; Fig 5B; 68pp; English.  
 CC This sequence is the antibody LD1-117-VL chain sequence, which is a  
 CC polypeptide of the invention. The polypeptides are capable of forming  
 CC antigen binding structures with specificity for Rhesus D antigens which  
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
 CC variable heavy (VH) and variable light (VL) chain sequences. The  
 CC antibodies are active against the Rhesus D antigen. They can be used for  
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
 CC protection of Rhesus negative women before or immediately after the birth  
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn  
 CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
 CC immunoglobulin can be used after transfusions of Rhesus positive blood  
 CC to Rhesus negative recipients in order to prevent sensitisation to the  
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
 SQ Sequence 106 AA;

Query Match 100.0%; Score 63; DB 29; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 mtqspsslas 12  
 |||||||||  
 QY 24 MTQSPSSLAS 34

RESULT 12  
 ID W22412 standard; Protein: 106 AA.

AC W22412:  
 DE 08-DEC-1997 (first entry)  
 KW Humanised alpha-4 integrin antibody 21.6 VL Ia.  
 KW Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;  
 KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;  
 KW metastasis; inflammatory bowel disease; rheumatoid arthritis;  
 KW transplant rejection; graft versus host disease; nephritis;  
 KW atopic dermatitis; psoriasis; myocardial ischaemia;  
 KW acute leukocyte mediated lung injury; therapy.  
 KW Chimeric Homo sapiens;  
 OS Chimeric Homo sapiens;  
 FH Chimeric synthetic.  
 FH Key  
 FT Location/Qualifiers  
 FT 1..23  
 FT /label= FR1  
 FT /note= "REI framework region 1"  
 FT 24..34  
 FT /label= CDR1  
 FT /note= "21.6 complementarity determining region 1"  
 FT 35..49  
 FT /label= FR2  
 FT /note= "REI framework region 2"  
 FT 45  
 FT /note= "REI framework region 2"  
 FT 45  
 FT /note= "REI Lys-45 is substd. by Lys of mouse  
 FT 21.6 VL, important in supporting the  
 FT CDR2 loop"  
 FT misc\_difference 49  
 FT /note= "REI Tyr-49 is substd. by His of mouse  
 FT 21.6 VL, located at the binding site"  
 FT 50..56  
 FT /label= CDR2  
 FT /note= "21.6 complementarity determining region 2"  
 FT 57..88  
 FT /label= FR3

FT /note= "REI framework region 3"  
 FT 58  
 FT /note= "REI Val-58 is substd. by Ile of mouse  
 FT 21.6 VL, important in supporting the CDR2  
 FT loop"  
 FT misc\_difference 69  
 FT /note= "REI Thr-69 is substd. by Arg of mouse  
 FT 21.6 VL, involved in antibody-antigen  
 FT binding"  
 FT 89..96  
 FT /label= CDR3  
 FT /note= "21.6 complementarity determining region 3"  
 FT 97..106  
 FT /label= FR4  
 FT /note= "REI framework region 4"  
 FT 103  
 FT /note= "REI Leu-103 substd. by Val, more typical  
 FT of human kappa light chain J region"  
 FT misc\_difference 104  
 FT /note= "REI Gln-104 substd. by Glu, more typical  
 FT of human kappa light chain J region"  
 FT 106  
 FT /note= "REI Thr-106 substd. by Lys, more typical  
 FT of human kappa light chain J region"  
 FT /note= "REI framework region 5"

MO9718838-A1.

PD 29-MAY-1997. U18807.  
 PF 21-NOV-1996; U18807.  
 PR (ATHE-) ATHENA NEUROSCINCES INC.  
 PA Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;  
 DR WPI: 97-297879/27.  
 PR Uses of humanised alpha-4 integrin antibody - for treatment of  
 PS asthma, atherosclerosis, AIDS, dementia, etc.  
 PS Claim 25; Fig 6; 107pp; English.  
 CC This polypeptide, designated Ia, comprises the light chain variable  
 CC region (VL) of a humanised alpha-4 integrin antibody 21.6. It is  
 CC composed of complementarity determining regions (CDRs) from the VL  
 CC region (see W22409) of mouse alpha-4 integrin monoclonal antibody  
 CC 21.6 and a modified human REI framework. It can be expressed in  
 CC mammalian host cells following PCR amplification and mutagenesis  
 CC of appropriate fragments of mouse and human DNA sequences. The  
 CC humanised 21.6 VL and a humanised 21.6 VH (see W22413) can be used  
 CC to produce a claimed humanised 21.6 antibody that is useful in the  
 CC manufacture of a medicament for treating asthma, atherosclerosis,  
 CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid  
 CC arthritis, transplant rejection, graft versus host disease, tumour  
 CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial  
 CC ischaemia, and acute leukocyte mediated lung injury. The antibody  
 CC may also be used in the affinity purification of alpha-4 integrin  
 CC for use as a vaccine or an immunogen. It is also useful for  
 CC generating idiotypic antibodies. The humanised antibody has a  
 CC half-life in the human circulation essentially equivalent to that  
 CC of naturally occurring human antibodies.  
 SQ Sequence 106 AA;

Query Match 100.0%; Score 63; DB 24; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 4 mtqspsslas 14  
 |||||||||  
 QY 24 MTQSPSSLAS 34

RESULT 13  
 ID W41390 standard; Protein: 107 AA.

AC W41390:  
 DE 02-JUN-1998 (first entry)  
 KW Anti-CER antibody; light chain variable region VK4.  
 KW Anti-CER antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;  
 KW cancer diagnosis; complementarity determining region; light chain.  
 KW synthetic.  
 OS WO9742329-A1.

PD 13-NOV-1997.  
 PF 29-APR-1997; G01165.  
 PR 14-FEB-1997; GB-003103.  
 PR 04-MAY-1996; GB-009405.  
 PA (ZENE ) ZENECA LTD.  
 PI Copley CG, Edge MD, Emery SC;  
 DR WPI; 97-558987/51.  
 DR N-PSDB; V17272.  
 PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for  
 diagnosis and therapy of cancer  
 CC Claim 4; Page 138-139; 208pp; English.  
 CC This sequence is the light chain variable region of the antibody of  
 the invention. The antibody is an anti-CEA (carcinoembryonic antigen)  
 antibody (806.077 Ab). Host cells or transgenic organisms transformed  
 CC with DNA encoding the antibody, are used to make the antibody or  
 CC conjugate. The conjugate is used in a medicament suitable for intravenous  
 CC administration. The conjugate can be used for cancer therapy, selectively  
 CC killing tumour cells. The antibody can be used for in vivo or in vitro  
 CC diagnosis of cancer.  
 Sequence 107 AA;

Query Match 100.0%; Score 63; DB 29; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 4 mtgspsslsas 14  
 |||||  
 OY 24 MTQSPSSLSAS 34

RESULT 14  
 ID W41397 standard; Protein; 107 AA.  
 AC W41397;  
 DT 02-JUN-1998 (first entry)  
 DE Anti-CEA antibody 806.077 variable light chain.  
 KM Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;  
 OS cancer diagnosis; complementarity determining region; Fd chain.  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Mus sp.  
 PN MO9742329-A1.  
 PD 13-NOV-1997.  
 PF 29-APR-1997; G01165.  
 PR 14-FEB-1997; GB-003103.  
 PR 04-MAY-1996; GB-009405.  
 PA (ZENE ) ZENECA LTD.  
 PI Copley CG, Edge MD, Emery SC;  
 DR WPI; 97-558987/51.  
 DR N-PSDB; V17296.  
 PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for  
 diagnosis and therapy of cancer  
 CC Example 11; Page 122-123; 208pp; English.  
 CC This sequence is the light chain variable region of the antibody of  
 CC the invention. The antibody is an anti-CEA (carcinoembryonic antigen)  
 CC antibody (806.077 Ab). Host cells or transgenic organisms transformed  
 CC with DNA encoding the antibody, are used to make the antibody or  
 CC conjugate. The conjugate is used in a medicament suitable for intravenous  
 CC administration. The conjugate can be used for cancer therapy, selectively  
 CC killing tumour cells. The antibody can be used for in vivo or in vitro  
 CC diagnosis of cancer.  
 Sequence 107 AA;

Query Match 100.0%; Score 63; DB 29; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 mtgspsslsas 14  
 |||||  
 OY 24 MTQSPSSLSAS 34

RESULT 15  
 ID W23953 standard; Protein; 107 AA.  
 AC W23953;

DE 17-JUN-1998 (first entry)  
 DE Chimeric humanised Mus musculus A717 antibody heavy chain.  
 KM Chimeric humanised; human; murine; A717; antibody; heavy chain;  
 KW variable region; diabetes; prophylactic treatment.  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 PN MO974429-A1.  
 PD 31-DEC-1997.  
 PF 26-JUN-1997; U11605.  
 PR 27-JUN-1996; US-672176.  
 PA (EXOC-) EXOCCEL INC.  
 PI Cohen MP, Shearman CW;  
 DR WPI; 98-076916/07.  
 DR N-PSDB; V04637.  
 PT New humanised antibodies specific for glycated albumin - prepared by  
 PT recombinant expression of humanised mouse antibodies, useful for,  
 PT e.g. treating diabetic vasculopathy  
 PS Example 2; Page 15; 27pp; English.  
 CC The sequence is that of a humanised variable region of the A717  
 CC antibody light chain VL-1. The antibody has specificity for glycated  
 CC albumin (GA) and is capable of neutralising the effects of GA in vivo.  
 CC It can be used in the manufacture of therapeutics useful for the  
 CC prophylactic treatment of complications of diabetes (especially  
 CC diabetic vasculopathy and retinopathy) and atherosclerotic  
 CC cardiovascular disease. The genetically engineered antibodies  
 CC are specific as they only interact with GA but not other proteins  
 CC and may be easily prepared in pure form.  
 Sequence 107 AA;

Query Match 100.0%; Score 63; DB 29; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 4 mtgspsslsas 14  
 |||||  
 OY 24 MTQSPSSLSAS 34

Search completed: Tue Apr 20 14:04:37 1999  
 Job time : 15 secs.



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 WISE (TM)  
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MPsrch.p protein - protein database search, using Smith-Waterman algorithm  
 on: Tue Apr 20 14:03:38 1999; Maspar time 3.28 Seconds  
 125.736 Million cell updates/sec  
 Tabular output not generated.

Title: >US-08-836-455-1\_1  
 Description: (24-34) from trans.dep (1 of 3)  
 Perfect Score: 63  
 Sequence: 1 MTQSPSSLSAS 11

Scoring table: PAM 150  
 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: plr58  
 1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 21.222; Variance 25.990; scale 0.817

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	63	100.0	53	2	PH0881	Ig kappa chain V reg1 1.28e-03
2	63	100.0	57	2	PH0879	Ig kappa chain V reg1 1.28e-03
3	63	100.0	62	2	S42265	Ig kappa chain V reg1 1.28e-03
4	63	100.0	94	2	PH1063	Ig kappa chain V reg1 1.28e-03
5	63	100.0	97	2	PH1064	Ig kappa chain V reg1 1.28e-03
6	63	100.0	103	2	S26332	Ig kappa chain V reg1 1.28e-03
7	63	100.0	104	2	S26330	Ig kappa chain V reg1 1.28e-03
8	63	100.0	106	2	PC2397	anti-tetanus toxin 9F 1.28e-03
9	63	100.0	106	2	C33936	Ig kappa chain V reg1 1.28e-03
10	63	100.0	106	2	PL0259	Ig kappa chain V reg1 1.28e-03
11	63	100.0	106	2	PL0260	Ig kappa chain V reg1 1.28e-03
12	63	100.0	107	2	S40366	Ig kappa chain V-J re 1.28e-03
13	63	100.0	107	2	S36275	Ig kappa chain V reg1 1.28e-03
14	63	100.0	107	2	S36262	Ig kappa chain V reg1 1.28e-03
15	63	100.0	107	2	S36269	Ig kappa chain V reg1 1.28e-03
16	63	100.0	107	2	JI0139	Ig kappa chain V reg1 1.28e-03
17	63	100.0	108	2	S36279	Ig kappa chain V reg1 1.28e-03
18	63	100.0	109	2	S31983	Ig kappa chain V reg1 1.28e-03
19	63	100.0	109	2	S31988	Ig kappa chain - huma 1.28e-03
20	63	100.0	109	2	S31979	Ig kappa chain - huma 1.28e-03
21	63	100.0	109	2	S31981	Ig kappa chain - huma 1.28e-03
22	63	100.0	109	2	S32001	Ig kappa chain - huma 1.28e-03
23	63	100.0	110	2	S44118	Ig kappa chain V-J re 1.28e-03

Result	1	ALIGNMENTS
24	63	100.0 116 2 A27594
25	63	100.0 117 2 S42263
26	63	100.0 117 2 S41809
27	63	100.0 117 2 S21658
28	63	100.0 117 2 S42264
29	63	100.0 117 2 S24206
30	63	100.0 117 2 C21056
31	63	100.0 117 2 B21056
32	63	100.0 120 2 S21665
33	63	100.0 120 2 S21667
34	63	100.0 122 2 S40314
35	63	100.0 123 2 S40354
36	63	100.0 123 2 S40313
37	63	100.0 123 2 S40313
38	63	100.0 125 2 S09365
39	63	100.0 125 2 S40353
40	63	100.0 125 2 S40350
41	63	100.0 125 2 S40315
42	63	100.0 126 2 S40335
43	63	100.0 127 2 S40367
44	63	100.0 129 2 S40369
45	63	100.0 135 2 S24320

ENTRY 1  
 TITLE PH0881 #type fragment  
 I g kappa chain V region (GOU) - human (fragment)  
 ALTERNATE\_NAMES myeloma protein  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 09-May-1997

ACCESSIONS  
 REFERENCE PH0881  
 #authors Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.;

#journal J. Exp. Med. (1991) 174:1639-1652  
 #title Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.  
 #cross-references M0UD:9207875

#accession PH0881  
 #molecule-type protein  
 #residues 1-53 #label MAN  
 CLASSIFICATION #superfamily Immunoglobulin V region; immunoglobulin homology heterotrimer; immunoglobulin

KEYWORDS  
 FEATURE 1-23 #region framework 1\  
 24-34 #region complementarity-determining 1\  
 35-49 #region framework 2\  
 50-53 #region complementarity-determining 2

SUMMARY  
 Query Match 100.0%; Score 63; DB 2; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 1.28e-03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTQSPSSLSAS 14  
 Qy 24 MTQSPSSLSAS 34

RESULT 2  
 ENTRY PH0879 #type fragment  
 TITLE I g kappa chain V region (MAR) - human (fragment)  
 ALTERNATE\_NAMES myeloma protein  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 09-May-1997  
 ACCESSIONS PH0879  
 REFERENCE PH0862  
 #authors Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.;

#journal J. Exp. Med. (1991) 174:1639-1652  
#title Molecular characteristics of antibodies bearing an  
anti-DNA-associated idiotype.  
#cross-references M01D:92078875  
#accession PH0879  
#molecule\_type protein  
#residues 1-57 #label MAN  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
FEATURE  
1-23 #region framework 1\  
24-34 #region complementarity-determining 1\  
35-49 #region framework 2\  
50-56 #region complementarity-determining 2  
SUMMARY #length 57 #checksum 6305

Query Match 100.0%; Score 63; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 1.28e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 4 MTOSPSLSAS 14  
OY 24 MTOSPSLSAS 34

RESULT 3  
ENTRY S42265 #type complete  
TITLE Ig kappa chain V region (018) - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change  
09-May-1997  
ACCESSIONS S42265  
REFERENCE Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.;  
Schaeble, K.F.; Thlebe, R.; Quenzel, E.M.; Zachau, H.G.;  
Nahm, M.H.  
#journal J. Immunol. (1991) 147:4007-4013  
#title Clonal characterization of the human IgG antibody repertoire  
to Haemophilus influenzae type b polysaccharide. IV. The  
less frequently expressed VL are heterogeneous.  
#accession S42265  
#status Preliminary  
#molecule\_type DNA  
#residues 1-62 #label SCO  
#cross-references EMBL:M64856

GENETICS  
#introns 19/1  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SUMMARY #length 62 #molecular\_weight 6821 #checksum 8574

Query Match 100.0%; Score 63; DB 2; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.28e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 4 MTOSPSLSAS 14  
OY 24 MTOSPSLSAS 34

RESULT 4  
ENTRY PH1063 #type fragment  
TITLE Ig light chain V region (clone 202.33) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change  
15-Jun-1996  
ACCESSIONS PH1063  
REFERENCE Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. (1992) 176:761-779  
Both IgM and IgG anti-DNA antibodies are the products of  
clonally selective B cell stimulation in (NZB x NZM)F1  
mice.

#accession PH1063  
#status nucleic acid sequence not shown  
#molecule\_type mRNA  
#residues 1-94 #label TIL  
#experimental\_source B cell, strain [NZB x NZM]F1  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
SUMMARY #length 94 #checksum 1938

Query Match 100.0%; Score 63; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 1.28e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 4 MTOSPSLSAS 14  
OY 24 MTOSPSLSAS 34

RESULT 5  
ENTRY PH1064 #type fragment  
TITLE Ig light chain V region (clone 202.54) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change  
15-Jun-1996  
ACCESSIONS PH1064  
REFERENCE PH0971  
Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. (1992) 176:761-779  
Both IgM and IgG anti-DNA antibodies are the products of  
clonally selective B cell stimulation in (NZB x NZM)F1  
mice.

#accession PH1064  
#status nucleic acid sequence not shown  
#molecule\_type mRNA  
#residues 1-97 #label TIL  
#experimental\_source B cell, strain [NZB x NZM]F1  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
SUMMARY #length 97 #checksum 1339

Query Match 100.0%; Score 63; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 1.28e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 4 MTOSPSLSAS 14  
OY 24 MTOSPSLSAS 34

RESULT 6  
ENTRY S26332 #type fragment  
TITLE Ig light chain V region - mouse (fragment)  
ALTERNATE\_NAMES Ig kappa chain V region  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change  
03-Aug-1998  
ACCESSIONS S26332; S26331  
REFERENCE S26309  
Stark, S.E.; Caton, A.J.  
J. Exp. Med. (1991) 174:613-624  
Antibodies that are specific for a single amino acid  
interchange in a protein epitope use structurally distinct  
variable regions.  
#accession S26332  
#molecule\_type mRNA  
#residues 1-103 #label STRA  
#cross-references EMBL:X59187; NID:952318; PID:636167; PID:91334064  
#note the sequence of residues 1-8 and the corresponding  
nucleic acid sequence are not shown

#accession S26331  
#status Preliminary  
#molecule\_type mRNA  
#residues 1-103 #label STR2

##cross-references EMBL:X59191; NID:g52321; PID:e36171; PID:g1334066  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SUMMARY #length 103 #checksum 1197

Query Match 100.0%; Score 63; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 1.28e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTOSPSLSAS 14  
OY 24 MTOSPSLSAS 34

RESULT 7  
ENTRY S26330 #type complete  
TITLE Ig kappa chain V region - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 08-Sep-1997

ACCESSIONS S26330  
REFERENCE S26309  
#authors Stark, S.E.; Caton, A.J.  
#journal J. Exp. Med. (1991) 174:613-624  
#title Antibodies that are specific for a single amino acid interchange in a protein epitope use structurally distinct variable regions.

#accession S26330  
#status preliminary  
#molecule\_type mRNA  
#residues 1-104 #label STA  
##cross-references EMBL:X59185; NID:g52316; PID:e36165; PID:g1334063  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SUMMARY #length 104 #molecular\_weight 11443 #checksum 4741

Query Match 100.0%; Score 63; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.28e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTOSPSLSAS 14  
OY 24 MTOSPSLSAS 34

RESULT 8  
ENTRY PC2397 #type fragment  
TITLE anti-tetanus toxin 9F12 Fab light-chain - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 13-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 16-Feb-1997

ACCESSIONS PC2397  
REFERENCE PC2397  
#authors Esposito, G.; Scarselli, E.; Traboni, C.  
#journal Gene (1994) 148:167-168  
#title Phage display of a human antibody against Clostridium tetani toxin.

#accession PC2397  
#molecule\_type mRNA  
#residues 1-106 #label ESP  
##cross-references EMBL:X75387  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
FEATURE 24-34 #region complementarity determining region 1  
50-56 #region complementarity determining region 2  
SUMMARY #length 106 #checksum 4925

Query Match 100.0%; Score 63; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.28e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTOSPSLSAS 14  
OY 24 MTOSPSLSAS 34

OY 24 MTOSPSLSAS 34

RESULT 9  
ENTRY C33936 #type fragment  
TITLE Ig kappa chain V region (VM113) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 08-Sep-1997

ACCESSIONS C33936  
REFERENCE A33936  
#authors Meek, K.; Johansson, B.; Schuman, J.; Bona, C.; Capra, J.D.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:4664-4668  
#title Nucleotide changes in sequential variants of influenza virus hemagglutinin genes and molecular structures of corresponding monoclonal antibodies specific for each variant.

#cross-references NID:89282831  
#accession C33936  
#status preliminary  
#molecule\_type mRNA  
#residues 1-106 #label MEE  
##cross-references GB:J04577; NID:g623187; PID:g623189  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SUMMARY #length 106 #checksum 2278

Query Match 100.0%; Score 63; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.28e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTOSPSLSAS 14  
OY 24 MTOSPSLSAS 34

RESULT 10  
ENTRY PLO259 #type fragment  
TITLE Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

ACCESSIONS PLO259  
REFERENCE PLO231  
#authors Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Weigert, M.  
#journal J. Exp. Med. (1990) 171:265-297  
#title Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.

#cross-references NID:90111618  
#accession PLO259  
#molecule\_type mRNA  
#residues 1-106 #label SHL  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
FEATURE 1-23 #region framework 1  
24-34 #region complementarity-determining 1  
35-49 #region framework 2  
50-56 #region complementarity-determining 2  
57-88 #region framework 3  
89-97 #region complementarity-determining 3  
98-106 #region framework 4  
SUMMARY #length 106 #checksum 2162

Query Match 100.0%; Score 63; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.28e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTOSPSLSAS 14  
OY 24 MTOSPSLSAS 34

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RESULT      11
ENTRY       PI0260    #type fragment
TITLE       Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
ORIGINISM   #formal_name Mus musculus #common_name house mouse
DATE        16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
          16-Aug-1996

ACCESSIONS  PI0260
REFERENCE    PI0231
#authors     Shlomchik, M.; Masceilli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
#journal     J. Exp. Med. (1990) 171:265-297
#title       Anti-DNA antibodies from autoimmune mice arise by clonal
             expansion and somatic mutation.
#cross-references MIMD:90111618
#accession   PI0260
##molecule_type mRNA
##residues   1-106 #label SHL
#superfamily immunoglobulin V region; immunoglobulin homology
heterotrimer; immunoglobulin

FEATURES
1-23
24-34
35-49
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57-88
89-97
98-106
SUMMARY      #length 106 #checksum 2157

Query Match      100.0%; Score 63; DB 2; Length 106;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      4 MTQSPSSLAS 14
|||||||
OY      24 MTQSPSSLAS 34

RESULT      12
ENTRY       S40366    #type complete
TITLE       Ig kappa chain V-J region - human
ORIGINISM   #formal_name Homo sapiens #common_name man
DATE        19-May-1994 #sequence_revision 26-May-1995 #text_change
          20-Mar-1998

ACCESSIONS  S40366
REFERENCE    S40312
#authors     Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal     Eur. J. Immunol. (1993) 23:3248-3271
#title       Expressed human immunoglobulin chl genes and their
             hypermutation.
#accession   S40366
#status      preliminary; translation not shown
#molecule_type mRNA
##residues   1-107 #label KLE
##cross-references EMBL:X72476; NID:g441420; PID:g441421
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS     heterotrimer; immunoglobulin
SUMMARY      #length 107 #molecular-weight 11556 #checksum 9149

Query Match      100.0%; Score 63; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      16 MTQSPSSLAS 26
|||||||
OY      24 MTQSPSSLAS 34

RESULT      13
ENTRY       S36275    #type fragment
TITLE       Ig lambda chain V region (clone alpha-FOG1-A4) - human

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ORGANISM
DATE
#formal_name Homo sapiens #common_name man
03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
08-Sep-1997

ACCESSIONS
REFERENCE
#authors
S36275
S36256
Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
Embleton, M.J.; McCafferty, J.; Baler, M.; Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
G.

#journal
#title
EMBO J. (1993) 12:725-734
Human anti-self antibodies with high specificity from phage
display libraries.

#accession
#status
#molecule_type mRNA
#residues
#cross-references EMBL:Z18827; NID:933416; PID:933909
CLASSIFICATION
#superfamily Immunoglobulin V region; immunoglobulin homology;
KEYWORDS
heterotetramer; immunoglobulin
length 107 #checksum 8985
SUMMARY

Query Match 100.0%; Score 63; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1,28e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTQSPSSLSAS 14
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OY 24 MTQSPSSLSAS 34

RESULT 14
ENTRY
TITLE
S36262 #type fragment
Ig lambda chain V region (clone alpha-TNF-E7) - human
(fragment)
ORGANISM
DATE
#formal_name Homo sapiens #common_name man
03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
16-Aug-1996

ACCESSIONS
REFERENCE
#authors
S36262
S36256
Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
Embleton, M.J.; McCafferty, J.; Baler, M.; Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
G.

#journal
#title
EMBO J. (1993) 12:725-734
Human anti-self antibodies with high specificity from phage
display libraries.

#accession
#status
#molecule_type mRNA
#residues
#cross-references EMBL:Z18842
CLASSIFICATION
#superfamily Immunoglobulin V region; immunoglobulin homology
KEYWORDS
heterotetramer; immunoglobulin
length 107 #checksum 4341
SUMMARY

Query Match 100.0%; Score 63; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1,28e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTQSPSSLSAS 14
|||||
OY 24 MTQSPSSLSAS 34

RESULT 15
ENTRY
TITLE
S36269 #type fragment
Ig lambda chain V region (clone alpha-TNF-A1) - human
(fragment)
ORGANISM
DATE
#formal_name Homo sapiens #common_name man
03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
08-Sep-1997

ACCESSIONS
REFERENCE
S36269
S36256

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#authors Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;  
Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;  
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,  
G.  
#journal EMBO J. (1993) 12:725-734  
#title Human anti-self antibodies with high specificity from phage  
display libraries.  
#accession S36269  
#status preliminary; nucleic acid sequence not shown  
#molecule\_type mRNA  
#residues 1-107 #label GRI  
#cross-references EMBL:Z18838; NID:93422; PID:939915  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotrimer; immunoglobulin  
SUMMARY #length 107 #checksum 6368  
Query Match 100.0%; Score 63; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.28e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
4 MTQSPSSLSAS 14  
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QY 24 MTQSPSSLSAS 34

Search completed: Tue Apr 20 14:04:04 1999  
Job time : 26 secs.

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1 MTQSPSSLAS 11

Gap 11

74019 seqs, 26840295 residues

Listing first 45 summaries

1:swissprot

Mean 21.723; Variance 21.843; scale 0.994

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description	Pred. No.
1	63	100.0	108	1	IG KAPPA CHAIN V-I REG	4.67e-03
2	63	100.0	108	1	IG KAPPA CHAIN V-I REG	4.67e-03
3	63	100.0	108	1	IG KAPPA CHAIN V-I REG	4.67e-03
4	63	100.0	108	1	IG KAPPA CHAIN V-I REG	4.67e-03
5	63	100.0	108	1	IG KAPPA CHAIN V-I REG	4.67e-03
6	63	100.0	108	1	IG KAPPA CHAIN V-I REG	4.67e-03
7	63	100.0	108	1	IG KAPPA CHAIN V-I REG	4.67e-03
8	63	100.0	108	1	IG KAPPA CHAIN V-I REG	4.67e-03
9	63	100.0	108	1	IG KAPPA CHAIN V-I REG	4.67e-03
10	63	100.0	108	1	IG KAPPA CHAIN V-I REG	4.67e-03
11	63	100.0	108	1	IG KAPPA CHAIN V-I REG	4.67e-03
12	63	100.0	109	1	IG KAPPA CHAIN V-I REG	4.67e-03
13	63	100.0	117	1	IG KAPPA CHAIN PRECURS	4.67e-03
14	63	100.0	117	1	IG KAPPA CHAIN PRECURS	4.67e-03
15	63	100.0	129	1	IG KAPPA CHAIN PRECURS	4.67e-03
16	63	100.0	129	1	IG KAPPA CHAIN PRECURS	4.67e-03
17	63	100.0	130	1	IG KAPPA CHAIN PRECURS	4.67e-03
18	61	96.8	107	1	IG KAPPA CHAIN V-I REG	1.78e-04
19	61	96.8	108	1	IG KAPPA CHAIN V-I REG	1.78e-04
20	61	96.8	108	1	IG KAPPA CHAIN V-I REG	1.78e-04
21	61	96.8	108	1	IG KAPPA CHAIN V-I REG	1.78e-04
22	61	96.8	112	1	IG KAPPA CHAIN V-I REG	1.78e-04
23	61	96.8	115	1	IG KAPPA CHAIN PRECURS	1.78e-04

45	53	86.1	134	1	KV4C_HUMAN	IG KAPPA	CHAIN PRECURS	3.03e-020
44	53	86.1	131	1	KV4D_HUMAN	IG KAPPA	CHAIN PRECURS	3.03e-020
43	53	86.1	121	1	KV4O_HUMAN	IG KAPPA	CHAIN PRECURS	3.03e-020
42	53	86.1	114	1	KV4A_HUMAN	IG KAPPA	CHAIN V REG	3.03e-020
41	53	86.1	109	1	KV01_RAT	IG KAPPA	CHAIN V REG	3.03e-020
40	53	86.1	108	1	KV5J_MOUSE	IG KAPPA	CHAIN V-V REG	3.03e-020
39	53	86.1	108	1	KV5N_MOUSE	IG KAPPA	CHAIN V-V REG	3.03e-020
38	53	86.1	108	1	KV5M_MOUSE	IG KAPPA	CHAIN V-V REG	3.03e-020
37	53	86.1	108	1	KV5L_MOUSE	IG KAPPA	CHAIN V-V REG	3.03e-020
36	53	86.1	108	1	KV5I_MOUSE	IG KAPPA	CHAIN V-V REG	3.03e-020
35	55	87.3	129	1	KV5H_HUMAN	IG KAPPA	CHAIN V-V REG	8.70e-030
34	55	87.3	108	1	KV5M_MOUSE	IG KAPPA	CHAIN V-V REG	4.62e-030
33	56	88.9	108	1	KV1V_HUMAN	IG KAPPA	CHAIN V-I REG	4.52e-030
32	56	88.9	108	1	KV1S_HUMAN	IG KAPPA	CHAIN V-I REG	2.44e-030
31	57	90.5	108	1	KV1K_HUMAN	IG KAPPA	CHAIN V-I REG	2.44e-030
30	58	92.1	108	1	KV5T_MOUSE	IG KAPPA	CHAIN V-V REG	1.28e-030
29	58	92.1	108	1	KV5S_MOUSE	IG KAPPA	CHAIN V-V REG	1.28e-030
28	58	92.1	108	1	KV5R_MOUSE	IG KAPPA	CHAIN V-V REG	1.28e-030
27	58	92.1	108	1	KV5Q_MOUSE	IG KAPPA	CHAIN V-V REG	1.28e-030
26	59	93.7	108	1	KV1M_HUMAN	IG KAPPA	CHAIN V-I REG	6.67e-040
25	60	95.8	117	1	KV1C_HUMAN	IG KAPPA	CHAIN V-I REG	3.46e-040
24	61	96.8	117	1	KV1B_HUMAN	IG KAPPA	CHAIN PRECURS	1.78e-040

## ALIGNMENTS

RESULT	1	STANDARD;	PRT;	108 AA.
ID	RVLY_HUMAN			
AC	P80362;			
DT	01-NOV-1995 (REL. 32, CREATED)			
DT	01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)			
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN V-I REGION (WAT).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).			
RA	MEDLINE; 95086080.			
RA	HUANG D.-B., CHANG C.-H., AINSWORTH C., BRUENGER A.T., EULITZ M.,			
RA	SOLOMON A., STEVENS F.J., SCHIFFER M.;			
RL	BIOCHEMISTRY 33:14848-14857(1994).			
RN	[2]			
RP	SEQUENCE OF 1-35.			
RX	MEDLINE; 81267384.			
RA	STEVENS F.J., WESTHOLM F.A., PANAGIOTOPoulos N., SCHIFFER M.,			
RA	POPP R.A., SOLOMON A.;			
RL	J. MOL. BIOL. 147:185-193(1981).			
CC	-1- THIS IS A BENCE-JONES PROTEIN.			
DR	PDB: 1MTL: 01-NOV-94.			
KM	IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; 3D-STRUCTURE.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 34			
FT	DOMAIN 35 49			
FT	DOMAIN 50 56			
FT	DOMAIN 57 88			
FT	DOMAIN 89 97			
FT	DOMAIN 98 107			
FT	DISULFID 23 88			
FT	CONFLICT 30 31			
FT	NON_TER 108 108			
SO	SEQUENCE 108 AA; 11737 MW; 41A2388C CRC32;			
Query Match	100.0%;	Score 63;	DB 1;	Length 108;
Best Local Similarity	100.0%;	Pred. No. 4.67e-05;		
Matches 11;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Db	4 MTQSPSSLAS 14			
Oy	24 MTQSPSSLAS 34			
RESULT	2			

ID KVIQ\_HUMAN STANDARD: PRT: 108 AA.  
AC P01609;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-I REGION (SCW).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 75059271.  
RA EDLITZ M., HILSCHMANN N.;  
RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 355:842-866(1974).  
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
CC -1- THIS IS A BENGE-JONES PROTEIN.  
DR PIR: A01875; KIHOSW.  
DR HSSP; P01607; IIGM.  
IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.  
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DOMAIN 1057 1109  
DOMAIN 1058 1110  
DOMAIN 1059 1111  
DOMAIN 1060 1112  
DOMAIN 1061 1113  
DOMAIN 1062 1114  
DOMAIN 1063 1115  
DOMAIN 1064 1116  
DOMAIN 1065 1117  
DOMAIN 1066 1118  
DOMAIN 1067 1119  
DOMAIN 1068 1120  
DOMAIN 1069 1121  
DOMAIN 1070 1122  
DOMAIN 1071 1123  
DOMAIN 1072 1124  
DOMAIN 1073 1125  
DOMAIN 1074 1126  
DOMAIN



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CC -!- THIS IS A BENGE-JONES PROTEIN.
DR PIR: A01873; KIHWE.
DR PDB: 1REI; 17-FEB-84.
KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN; 3D-STRUCTURE.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 56 FRAMEWORK 3.
FT DOMAIN 6 57 FRAMEWORK 4.
FT DOMAIN 7 88 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 8 97 FRAMEWORK 1.
FT DISULFID 23 88
FT NON_TER 108 108
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 33 38
FT STRAND 40 41
FT STRAND 45 49
FT STRAND 50 52
FT STRAND 53 54
FT STRAND 56 57
FT STRAND 60 61
FT STRAND 62 67
FT STRAND 68 69
FT STRAND 70 75
FT STRAND 80 82
FT HELIX 85 90
FT STRAND 85 98
FT STRAND 98 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11902 MW; D08F51A4 CRC32;

Query Match
Best Local Similarity 100.0%; Score 63; DB 1; Length 108;
Pred. No. 4,67e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 4 MTQSPSSLSAS 14
QY 24 MTQSPSSLSAS 34

RESULT 6
ID KVIN_HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (OU).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN (1)
RP SEQUENCE.
RX MEDLINE: 70201507.
RA KOHLER H., SHIMIZU A., PAUL C., PUTNAM F.W.;
RL SCIENCE 169:56-59(1970).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DE -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
DR HSSP: P01607; 2FGW.
DR PIR: A01872; KIHOU.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 56 FRAMEWORK 3.
FT DOMAIN 6 57 FRAMEWORK 4.
FT DOMAIN 7 88 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 88
FT NON_TER 108 108
FT STRAND 108 AA; 11777 MW; 4B089785 CRC32;
SQ SEQUENCE

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Query Match
Best Local Similarity 90.9%; Score 63; DB 1; Length 108;
Pred. No. 4,67e-05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 4 MTQSPSSLSAS 14
QY 24 MTQSPSSLSAS 34

RESULT 7
ID KVIN_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (WEA).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN (1)
RP SEQUENCE.
RX MEDLINE: 83273707.
RA GONI F., FRANGIONE B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 80:4837-4841(1983).
CC -!- THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST
3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR: A01876; KIHWE.
DR HSSP: P01607; 2FGW.
KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 56 FRAMEWORK 3.
FT DOMAIN 6 57 FRAMEWORK 4.
FT DOMAIN 7 88 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; B8ADA251 CRC32;

Query Match
Best Local Similarity 100.0%; Score 63; DB 1; Length 108;
Pred. No. 4,67e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 4 MTQSPSSLSAS 14
QY 24 MTQSPSSLSAS 34

RESULT 8
ID KVIN_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (DEE).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN (1)
RP SEQUENCE.
RX MEDLINE: 72053133.
RA MILSTEIN C.P., DEVENSON E.V.;
RL BIOCHEM. J. 123:945-958(1971).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR: A01865; KIHWE.
DR HSSP: P01607; 1FVC.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 56 FRAMEWORK 3.
FT DOMAIN 6 57 FRAMEWORK 4.
FT DOMAIN 7 88 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE

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CC DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 107 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11661 MW; 1DE844F3 CRC32;

Query Match 100.0%; Score 63; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.67e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTQSPSSLSAS 14  
 |||||  
 OY 24 MTQSPSSLSAS 34

RESULT 9  
 KVIA\_HUMAN STANDARD; PRT; 108 AA.  
 P01593;

DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-I REGION (AG).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE; 69234734.  
 RA TITANI K., SHINODA T., PUTNAM F.W.;  
 CC J. BIOL. CHEM. 244:3550-3560(1969).  
 -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- THIS IS A BENGE-JONES PROTEIN.  
 DR PIR: A01861; KIHUAG.  
 DR HSP: P01607; IREI.  
 DR IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11992 MW; 225444C7 CRC32;

Query Match 100.0%; Score 63; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.67e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTQSPSSLSAS 14  
 |||||  
 OY 24 MTQSPSSLSAS 34

RESULT 10  
 KVIA\_HUMAN STANDARD; PRT; 108 AA.  
 P01600;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-I REGION (HAU).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE; 71032830.  
 RA MATANABE S., HILSCHMANN N.;  
 RA HOPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1291-1295(1970).  
 -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1- THIS IS A BENGE-JONES PROTEIN.  
 DR PIR: A01868; KIHUAG.  
 DR HSP: P01607; IFVC.  
 KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11671 MW; C8A2E86 CRC32;

Query Match 100.0%; Score 63; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.67e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTQSPSSLSAS 14  
 |||||  
 OY 24 MTQSPSSLSAS 34

RESULT 11  
 ID KVIB\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01594;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-I REGION (AU).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE; 72189444.  
 RA SCHIEHL H., HILSCHMANN N.;  
 RA HOPE-SEYLER S.Z. PHYSIOL. CHEM. 353:345-370(1972).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE; 77022433.  
 RA FEHLHÄMER H., SCHIFFER M., EPP O., COLMAN P.M., LATYMAN E.E.,  
 RA SCHWAGER P., STEIGEMANN W., SCHRAMM H.J.;  
 RA BIOPHYS. STRUCT. MECH. 1:139-146(1975).  
 CC -1- THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR  
 CC REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF  
 CC THE KAPPA CHAIN REI.

CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- THIS IS A BENGE-JONES PROTEIN.  
 DR PIR: A01862; KIHUAG.  
 DR HSP: P01607; IIGM.  
 DR IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11939 MW; B455AF00 CRC32;

Query Match 100.0%; Score 63; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.67e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTQSPSSLSAS 14  
 |||||  
 OY 24 MTQSPSSLSAS 34

RESULT 12  
ID KVL1\_HUMAN STANDARD; PRT; 109 AA.  
AC P01612;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DE 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-I REGION (MEV).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 83081018.  
RA EULITZ M., LINKE R.P.;  
RL HOPPE-SEYLER'S 2. PHYSIOL. CHEM. 363:1347-1358(1982).  
CC -1- ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO FOUND.  
CC -1- THIS CHAIN WAS ISOLATED FROM A MELOMA PROTEIN.  
DR HSP; A01879; KIHUMV.  
DR HSP; P01607; 2FGM.  
DR IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 2 34  
FT DOMAIN 3 49  
FT DOMAIN 4 50  
FT DOMAIN 5 56  
FT DOMAIN 6 57  
FT DOMAIN 7 88  
FT DOMAIN 8 98  
FT DOMAIN 9 99  
FT DISULFID 23 88  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA; 11870 MW; D724EC1 CRC32;  
Query Match 100.0%; Score 63; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred. No. 4.67e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 4 MTQSPSSLSAS 14  
QY 24 MTQSPSSLSAS 34  
RESULT 13  
ID KVS\_MOUSE STANDARD; PRT; 117 AA.  
AC P01641;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 173B).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 81064681.  
RA MAX E.E., SEIDMAN J.G., MILLER H., LEDER P.;  
RL CELL 21:793-799(1980).  
DR EMBL; K00880; G197444;  
DR PIR; A01924; KYMS3B.  
DR HSP; P01607; 1FGV.  
DR IMMUNOGLOBULIN V REGION; SIGNAL.  
KM SIGNAL 1 22  
FT CHAIN 23 117  
FT DOMAIN 23 45  
FT DOMAIN 46 56  
FT DOMAIN 57 71  
FT DOMAIN 72 78  
FT DOMAIN 79 110  
FT DOMAIN 111 >117  
FT DISULFID 45 110  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12954 MW; 38F2B08C CRC32;  
Query Match 100.0%; Score 63; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 4.67e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 26 MTQSPSSLSAS 36  
QY 24 MTQSPSSLSAS 34  
RESULT 14  
ID KVL1\_HUMAN STANDARD; PRT; 117 AA.  
AC P01601;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DE 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN PRECURSOR V-I REGION (HK101) (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 81098966.  
RA BENTLEY D.L., RABBITTS T.H.;  
RL NATURE 288:730-733(1980).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 83129397.  
RA BENTLEY D.L., RABBITTS T.H.;  
RL CELL 32:181-189(1983).  
DR EMBL; J00244; G185970;  
DR EMBL; K01322; G185984;  
DR EMBL; K01324; G185988;  
DR EMBL; V00558; G331177;  
DR PIR; A01881; KIHU11.  
DR PIR; A21056; A21056.  
DR HSP; P01607; 1DPB.  
DR IMMUNOGLOBULIN V REGION; SIGNAL.  
KM SIGNAL 1 22  
FT CHAIN 23 >117  
FT DOMAIN 23 45  
FT DOMAIN 46 56  
FT DOMAIN 57 71  
FT DOMAIN 72 78  
FT DOMAIN 79 110  
FT DOMAIN 111 >117  
FT DISULFID 45 110  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12799 MW; B02D3E1 CRC32;  
Query Match 100.0%; Score 63; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 4.67e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 26 MTQSPSSLSAS 36  
QY 24 MTQSPSSLSAS 34  
RESULT 15  
ID KVLX\_HUMAN STANDARD; PRT; 129 AA.  
AC P04432;  
DT 13-AUG-1987 (REL. 05, CREATED)  
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN PRECURSOR V-I REGION (DAIDI).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 85014148.  
RA KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;  
RL NUCLEIC ACIDS RES. 12:6995-7006(1984).  
DR EMBL; K02134; G185822;  
DR EMBL; X00966; G296685; ALT\_TERM.

Tue Apr 20 14:30:48 1999

DR PIR: A01884; KIHUOI.  
DR HSSP: P01607; IGV.  
KW IMMUNOGLOBULIN V REGION; SIGNAL.  
FT SIGNAL 1 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION (DAUDI).  
FT DOMAIN 23 45 FRAMEWORK 1.  
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 57 71 FRAMEWORK 2.  
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 79 110 FRAMEWORK 3.  
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 120 129 FRAMEWORK 4.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14235 MM; 05B40B5E CRC32;

Query Match 100.0%; Score 63; DB 1; Length 129;  
Best Local Similarity 100.0%; Pred. No. 4.67e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 26 MTQSPSSLSAS 36  
QY 24 MTQSPSSLSAS 34

Search completed: Tue Apr 20 14:02:24 1999  
Job time : 6 secs.

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generated:

1 MTQSPSSLSAS 11

## Gap 11

165420 seqs, 49795644 residues

existing first 45

sptrembl6

13:sp\_vertebrate 14:sp\_virus

mean 20.775; Variance 22.138; scale 0.938

ved by analysis of the total score distribution.

## SUMMARIES

	Accession	Gene	Length	Score	E-value	Description
5.2	112	4	Q99822	ANTI-HIV-1 GP120 ANTIB	1.06e+00	

45	43	68.3	1517	2	034071	ORF40.	1.62e+01
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## ALIGNMENTS

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ID RESULT 1 PRELIMINARY; PRT; 50 AA.
AC 015533
AC 015533:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE DNA REARRANGED BY A T(2;8) TRANSLOCATION LEADING TO BURKITT'S LYMPHOMA
DE IN THE CELL LINE J1 (CLONE J1P) .
OS HOMO SAPIENS (HUMAN) .
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA KLOBECK H.G.;
RL SUBMITTED (AVG-1987) TO EMBL/GENBANK/DBJ DATA BANKS.
RP [2]
RP SEQUENCE OF 36-50 FROM N.A.
RX MEDLINE; 87259967.
RA KLOBECK H.G., COMERIATO G., ZACHAU H.G.;
RA NUCLEIC ACIDS RES. 15:4877-4888(1987) .
DR EMBL; X05929; E12675; -.
SQ SEQUENCE 50 AA; 5486 MW; 65586C19 CRC32;

Query Match 100.0%; Score 63; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. NO. 1.08e-04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db 7 MTOSPPSLAS 17
      |||||
QY 24 MTOSPPSLAS 34

RESULT 2 PRELIMINARY; PRT; 105 AA.
ID 099514
AC 099514:
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE LIGHT CHAIN FAB FRAGMENT (FRAGMENT) .
OS HOMO SAPIENS (HUMAN) .
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.

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RA HORN M.P., VOGEL M., BIAGGI C., MIESCHER S.M., STADLER B.M.;  
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: Y08148; E274854; -

DR PFAM: PF00047; 19.

FT NON\_TER 1 1

FT NON\_TER 105 105

SO SEQUENCE 105 AA; 11303 MW; 249B7EC3 CRC32;

Query Match

Best Local Similarity 100.0%; Score 63; DB 4; Length 105;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 MTQSPSSLSAS 12

QY 24 MTQSPSSLSAS 34

RESULT 3

099980; PRELIMINARY; PRT; 107 AA.

099980; 01-MAY-1997 (TREMBLREL. 03, CREATED)

DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)

DE VASOACTIVE INTESTINAL POLYPEPTIDE HYDROLYZING AUTOANTIBODY LIGHT CHAIN (FRAGMENT).

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RA TYTYULKOVA S., GAO Q.S., THOMPSON A., RENNARD S., PAUL S.;

RL BIOCHIM. BIOPHYS. ACTA 1316:217-223(1996).

DR EMBL: L43498; G1850120; -

DR PFAM: PF00047; 19.

FT NON\_TER 1 1

FT NON\_TER 107 107

SO SEQUENCE 107 AA; 11825 MW; C1E164AA CRC32;

Query Match

Best Local Similarity 100.0%; Score 63; DB 4; Length 107;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 MTQSPSSLSAS 14

QY 24 MTQSPSSLSAS 34

RESULT 4

099953; PRELIMINARY; PRT; 107 AA.

099953; 01-MAY-1997 (TREMBLREL. 03, CREATED)

DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)

DE VASOACTIVE INTESTINAL POLYPEPTIDE HYDROLYZING AUTOANTIBODY LIGHT CHAIN (FRAGMENT).

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RA TYTYULKOVA S., GAO Q.S., THOMPSON A., RENNARD S., PAUL S.;

RL BIOCHIM. BIOPHYS. ACTA 1316:217-223(1996).

DR EMBL: L43499; G1850134; -

OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
OC EUTHERIA; PRIMATES.  
RN  
RP SEQUENCE FROM N.A.  
RA ERMEL R.M., KENNY T.P., CHEN P.P., ROBBINS D.L.,  
RL ARTHURIS RHEUM. (MUNCH.) 36:380-388(1993).  
DR EMBL; S56182; G298561.  
PEAM; PF00047; 19.  
FT NON\_TER 1 1  
FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 12528 MW; BFFBD90D CRC32;  
Query Match 96.88; Score 61; DB 4; Length 116;  
Best Local Similarity 90.98; Pred. No. 3.94e-04;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 4 MTOSPSLSAS 14  
|||||:||||  
24 MTOSPSLSAS 34  
RESULT 8  
ID 043690 PRELIMINARY; PRT; 239 AA.  
AC 043690;  
DT 01-JUN-1998 (TREMELREL. 06, CREATED)  
DT 01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMELREL. 06, LAST ANNOTATION UPDATE)  
DE ANTI-MPL SCFV (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
OC EUTHERIA; PRIMATES.  
RN  
RP SEQUENCE FROM N.A.  
RA GODDARD A., YUAN J., ZHU Z., CARTER P.,  
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL; AF048775; G2911502; -.  
FT NON\_TER 1 1  
FT NON\_TER 239 239  
SQ SEQUENCE 239 AA; 25262 MW; 5B9ABF4C CRC32;  
Query Match 96.88; Score 61; DB 4; Length 239;  
Best Local Similarity 90.98; Pred. No. 3.94e-04;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 136 MTOSPSLSAS 146  
|||||:||||  
24 MTOSPSLSAS 34  
RESULT 9  
ID 060289 PRELIMINARY; PRT; 240 AA.  
AC 000289;  
DT 01-JUL-1997 (TREMELREL. 04, CREATED)  
DT 01-JUL-1997 (TREMELREL. 04, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMELREL. 07, LAST ANNOTATION UPDATE)  
DE SINGLE-CHAIN FV FRAGMENT (FRAGMENT).  
GN SCFV.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
OC EUTHERIA; PRIMATES.  
RN  
RP SEQUENCE FROM N.A.  
RA KONTERMANN R.E., WING M.G., WINTER G.,  
RL NAT. BIOTECHNOL. 15:629-631(1997).  
DR EMBL; Y13056; E315281; -.  
PEAM; PF00047; 19.  
FT NON\_TER 1 1  
FT NON\_TER 240 240  
SQ SEQUENCE 240 AA; 25569 MW; 6472A9C9 CRC32;  
Query Match 96.88; Score 61; DB 4; Length 240;  
Best Local Similarity 90.98; Pred. No. 3.94e-04;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 136 MTOSPSLSAS 146  
|||||:||||  
24 MTOSPSLSAS 34  
Query Match 96.88; Score 61; DB 4; Length 244;  
Best Local Similarity 90.98; Pred. No. 3.94e-04;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 140 MTOSPSLSAS 150  
|||||:||||  
24 MTOSPSLSAS 34  
RESULT 11  
ID 043689 PRELIMINARY; PRT; 244 AA.  
AC 043689;  
DT 01-JUN-1998 (TREMELREL. 06, CREATED)  
DT 01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMELREL. 06, LAST ANNOTATION UPDATE)  
DE ANTI-HER3 SCFV (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
OC EUTHERIA; PRIMATES.  
RN  
RP SEQUENCE FROM N.A.  
RA GODDARD A., YUAN J., ZHU Z., CARTER P.,  
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL; AF048774; G2911500; -.  
FT NON\_TER 1 1  
FT NON\_TER 244 244  
SQ SEQUENCE 244 AA; 26025 MW; 47670049 CRC32;  
Query Match 96.88; Score 61; DB 4; Length 244;  
Best Local Similarity 90.98; Pred. No. 3.94e-04;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 141 MTOSPSLSAS 151  
|||||:||||  
24 MTOSPSLSAS 34  
RESULT 12  
ID 014540 PRELIMINARY; PRT; 113 AA.  
AC 014540;  
DT 01-JAN-1998 (TREMELREL. 05, CREATED)  
DT 01-JAN-1998 (TREMELREL. 05, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMELREL. 07, LAST ANNOTATION UPDATE)  
DE HIV FAB 027-VL (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUKARYOTA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PBL.  
 RA ITOH K., SUZUKI T.;  
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; AB006849; D1023047; -.  
 PFAM; PF00047; 19.  
 FT NON\_TER 113 113  
 SO SEQUENCE 113 AA; 12383 MW; FCEB1F02 CRC32;

Query Match  
 Best Local Similarity 90.9%; Score 60; DB 4; Length 113;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 6 MTOSPSLSAS 16  
 :|||||:  
 24 MTOSPSLSAS 34

RESULT 13  
 ID P97771 PRELIMINARY; PRT; 241 AA.  
 AC P97771;  
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)  
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE ANTI-CEA 79 SINGLE CHAIN TV FRAGMENT (FRAGMENT).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUKARYOTA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA CHUNG J.H., LEE S.D., YI K.S., SUH P.G., RYU S.H., CHOI S.J., KIM H.J.,  
 RL KIM I.J., CHOI I.H., CHUNG H.K.;  
 RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; U88067; G1850548; -.  
 PFAM; PF00047; 19.  
 FT NON\_TER 1 1  
 FT NON\_TER 241 241  
 SO SEQUENCE 241 AA; 26086 MW; EBB2D29D CRC32;

Query Match  
 Best Local Similarity 88.9%; Score 56; DB 11; Length 241;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

137 LTOSPSLSAS 147  
 :|||||:  
 24 MTOSPSLSAS 34

RESULT 14  
 ID Q99818 PRELIMINARY; PRT; 108 AA.  
 AC Q99818;  
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)  
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE ANTI-SSDNA ANTIBODY LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 GN HUMKV3285.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUKARYOTA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA SUENAGA R.;  
 RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; U82258; G1773057; -.  
 PFAM; PF00047; 19.  
 FT NON\_TER 1 1  
 FT NON\_TER 108 108  
 SO SEQUENCE 108 AA; 11792 MW; 876D5BA3 CRC32;

Query Match  
 87.3%; Score 55; DB 4; Length 108;

Best Local Similarity 72.7%; Pred. No. 1.70e-02;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 4 MTOSPATISVS 14  
 :|||||:  
 QY 24 MTOSPSLSAS 34

RESULT 15  
 ID P97408 PRELIMINARY; PRT; 102 AA.  
 AC P97408;  
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)  
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE TYPE II COLLAGEN ANTIBODY KAPPA LIGHT CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUKARYOTA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DBA/1J.  
 RX MEDLINE; 97257994.  
 RA ITO H.O., UEDA T., HASHIMOTO Y., IMOTO T., KOGA T.;  
 RL CELL. MOL. LIFE SCI. 53:51-60(1997).  
 DR EMBL; U69539; G1731667; -.  
 PFAM; PF00047; 19.  
 FT NON\_TER 1 1  
 FT NON\_TER 102 102  
 SO SEQUENCE 102 AA; 11093 MW; D3B638CD CRC32;

Query Match  
 Best Local Similarity 85.7%; Score 54; DB 11; Length 102;  
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 4 LTOSPTSLSAS 14  
 :|||||:  
 QY 24 MTOSPSLSAS 34

Search completed: Tue Apr 20 14:03:20 1999  
 Job time : 37 secs.



(W.I.)

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1 GINLHWL 7

Gap 11

Listing first 45 summaries

29:part29

Mean 16.909; Variance 67.405; scale 0.251

derived by analysis of the total score distribution.

## SUMMARIES

74.245

## ALIGNMENTS

PI Chatto

DR WPI: 97-341690/31.  
 DR N-PSDB: T85149.  
 PT Monoclonal anti-idiotype antibody 11D10 - elicits immune response  
 PT against human milk fat globule disease associated tumours,  
 PT especially breast cancer  
 PS Claim 9; Page 94; 130pp; English.  
 CC This polypeptide sequence comprises the light chain variable region  
 CC (VL) of monoclonal anti-idiotype antibody 11D10 produced by  
 CC hybridoma cell line ATCC 10220. 11D10 was obtained by immunising  
 CC naive mice with MC-10 anti-HMG antibody to obtain an anti-idiotype  
 CC response. It elicits an immune response against a specific epitope  
 CC of a high mol.wt. mucin of human milk fat globule (HMG). It  
 CC induces an immunological response to HMG in mice, rabbits, monkeys  
 CC and patients with advanced HMG-associated tumours. Pharmaceutical  
 CC compositions and vaccines comprising 11D10, 11D10 polypeptides  
 CC and/or 11D10 polynucleotides (see also T85149-50) are claimed.  
 CC Also claimed are diagnostic kits and methods of using 11D10, 11D10  
 CC polypeptides and/or 11D10 polynucleotides, including methods of  
 CC treating HMG-associated tumours. 11D10 is also used in a claimed  
 CC method of palliating HMG-associated disease and in claimed kits to  
 CC detect or quantify anti-HMG antibody.  
 SQ Sequence 145 AA;

Query Match 100.0%; Score 62; DB 25; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 2.56e+01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 50 gnlhw1 56  
 |||||  
 OY 50 GINLHWL 56

RESULT 2  
 ID R65017 standard; Protein; 1082 AA.  
 AC R65017;

DE 30-SEP-1995 (first entry)  
 DE PRB2 retinoblastoma tumour suppressor protein.  
 KM Retinoblastoma; tumour suppressor; PRB2; diagnostic.  
 OS Homo sapiens.

FT Key Location/Qualifiers  
 misc\_difference 507.512

FT FT /note="primer A (R65015) recognition site"  
 PN W09505470-A.

PD 23-FEB-1995.  
 PF 12-AUG-1994; U09293.  
 PR 12-AUG-1993; US-106493.

(UTEM) UNIV TEMPLE.  
 Giordano A;

WPI: 95-098768/13.  
 N-PSDB: Q82748.

PT DNA encoding retinoblastoma suppressor protein, PRB2 - and

PT recombinant cell lines, for the diagnosis and suppression of

PT cells infected with adenovirus E1A.

PS Claim 10; Page 19-22; 29pp; English.

CC The retinoblastoma tumour suppressor protein, PRB2, binds to the

CC E1A transforming domain, and is useful in the diagnosis of cells

CC infected with adenovirus E1A or a related virus. The protein

CC may be administered as a cell growth suppressor to infected cells

CC e.g. retinoblastoma interocular cancer cells, and may be useful

CC for identifying other DNA tumour virus oncoproteins.

SQ Sequence 1082 AA;

Query Match 80.6%; Score 50; DB 13; Length 1082;  
 Best Local Similarity 71.4%; Pred. No. 2.73e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 24 gnlhw1 30  
 | : |||||  
 OY 50 GINLHWL 56

RESULT 3  
 ID W45546 standard; peptide; 20 AA.

AC W45546;  
 DE 28-MAY-1998 (first entry)  
 DE N-acetylamino-alcohol hydrolase N-terminal amino acid fragment.  
 KM N-acetylamino-alcohol hydrolase; NAAH; cyclopentene; chiral;  
 KM carbon source; N-terminus.  
 OS Rhodococcus erythropolis.  
 PN W09745529-A1.

PD 04-DEC-1997.

PF 30-MAY-1997; E02838.

PR 18-APR-1997; CH-000908.

PR 30-MAY-1996; CH-001359.

PR 10-FEB-1997; CH-000282.

PA (LONZ) LONZA AG.

PI Bernegger-egli C, Birch OM, Bossard P, Brieden W,

PI Brux F, Burdorf K, Duc L, Etter K, Guggisberg I,

PI Sauter M, Urban EM;

DR WPI: 98-032639/03.

PT New microorganisms able to utilise specific acylamino cyclopentene

PT derivatives as carbon source - and derived N-acetylamino-alcohol

PT hydrolases, for preparation of chiral

PT 1-amino-4-hydroxymethyl-2-cyclopentene from N-acyl precursors

PS Claim 6; Page 54; 68pp; German.

CC This is the specifically claimed N-terminal amino acid sequence of

CC N-acetylamino-alcohol hydrolase from Rhodococcus erythropolis. The

CC invention relates to microorganisms, or their enzymatic extracts, able

CC to utilise cyclopentene derivatives as sole carbon (or carbon and

CC nitrogen) source. The invention also relates to new N-acetylamino-alcohol

CC hydrolases (NAAH) from the microorganisms for preparation of chiral

CC 1-amino-4-hydroxymethyl-2-cyclopentene from N-acyl precursors.

CC Compared with other methods, this method of preparation involves fewer

CC stages and does not require lithium aluminium hydride or other expensive

CC reagents.  
 SQ Sequence 20 AA;

Query Match 77.4%; Score 48; DB 29; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.00e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 4 nlhw1 8  
 |||||  
 OY 52 NLHWL 56

RESULT 4

ID R04101 standard; protein; 338 AA.  
 AC R04101;

DE 10-SEP-1990 (first entry)

DE Sequence encoding Isopenicillin N synthetase activity

KM Iso-penicillin N synthetase; Cephalosporin acromonium; antibiotic.

OS Cephalosporin acromonium.

PN AU8942347-A.

PD 11-JAN-1990.

PF 27-SEP-1989; -42347.

PR 01-JUN-1986; AU-042347.

PA (ELIL) Eli Lilly and Co.

PI Ingolia TD, Queener SH, Samson SM, Skatrud PL;

DR WPI: 90-124616/17.

DR N-PSDB: 004021.

PT Iso-penicillin N synthetase activating sequences isolated from DNA

PT from Cephalosporin acromonium and used to increase antibiotic prodn.

PS Disclosure; pp; English.

CC This enzyme can be used to produce isopenicillin N from the tripeptide

CC delta-(L-alpha-aminoacidyl)-L-cysteine-D-valine. Isopenicillin N is a

CC starting material for penicillin N and other cephalosporins. The greatest

CC potential use of the enzyme is to condense other tripeptides into novel

CC beta lactam derivatives.

CC See also 004022

SQ Sequence 338 AA;

Query Match 77.4%; Score 48; DB 1; Length 338;  
 Best Local Similarity 57.1%; Pred. No. 4.00e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 50 gvd1pw1 56  
|:::|  
QY 50 GINLHML 56

RESULT 5  
ID R03733 standard; protein: 338 AA.  
AC R03733:  
DT 24-JUL-1990 (first entry)  
DE Cephalosporium acremonium isopenicillin-N-synthetase.  
KW isopenicillin-N-synthetase; enzyme.  
OS Cephalosporium acremonium.  
PN US4885251-B.  
PD 05-DEC-1989.  
PF 08-AUG-1986; 895008.  
PR 08-AUG-1986; US-895008.  
PA (ELI) Eli Lilly & Co.  
PI Ingolia TD, Queener SW, Samson SM, Skatrud PL, Godfrey OW;  
DR WPI: 90-044769/06.  
N-PSDB: 003261.  
PT New recombinant DNA compounds encoding isopenicillin-N-synthetase -  
used to produce vectors for improving fermentation efficiency and  
yield of penicillin antibiotic-producing organisms, etc.  
PS Claim 4; page 25; 40pp; English.  
CC The protein is encoded in plasmid pPS19 and plasmid pS24.  
CC It has been used to construct novel E. coli expression  
CC vectors that drive expression of a stable, active, and novel  
CC isopenicillin-N-synthetase in E. coli. See also 003267.  
SQ Sequence 338 AA;

Query Match 77.4%: Score 48; DB 2; Length 338;  
Best Local Similarity 57.1%: Pred. No. 4.00e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 50 gvd1pw1 56  
|:::|  
QY 50 GINLHML 56

RESULT 6  
ID P60508 standard; protein: 339 AA.  
AC P60508:  
DT 24-MAY-1991 (first entry)  
DE isopenicillin N synthetase  
KW isopenicillin N synthetase.  
OS Cephalosporin acremonium.  
PN AV8656431-A.  
PD 30-OCT-1986.  
PF 21-APR-1986; 056431.  
PR 22-APR-1985; US-725870.  
PR 18-NOV-1985; US-799384.  
PR 08-AUG-1986; US-895008.  
PA (ELI) Eli Lilly & Co.  
PI Ingolia TD, Queener SW, Samson SM, Skatrud PL;  
DR WPI: 86-325839/50.  
N-PSDB: N60414.  
PT New DNA encoding iso-penicillin N synthetase - for use in vectors  
PT permitting high level expression, esp. in prodn. of penicillin  
PS Claim 28; page 86-7; 113pp; English.  
CC isopenicillin N synthetase (IPS) can be expressed using a vector  
CC which permits high level expression of IPS activity in E. coli. The  
CC IPS from E. coli forms isopenicillin N from delta-(L-alpha-aminoadipyl)  
CC L-cysteinyl-D-valine, and is also useful for condensing other  
CC tripeptides to form new antibiotics.  
SQ Sequence 339 AA;

Query Match 77.4%: Score 48; DB 3; Length 339;  
Best Local Similarity 57.1%: Pred. No. 4.00e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 50 gvd1pw1 56  
|:::|

QY 50 GINLHML 56

RESULT 7  
ID W22212 standard; Protein: 622 AA.  
AC W22212:  
DT 02-NOV-1997 (first entry)  
DE Rat transferrin receptor.  
KW Radiation; radiomimetic; exposure; transferrin receptor;  
KW red blood cell; rat.  
OS Rattus norvegicus.  
PN W09715830-A1.  
PD 01-MAY-1997.  
PF 21-OCT-1996; U16880.  
PR 24-OCT-1995; US-547197.  
PA (UNYNY) UNIV NEW YORK STATE RES FOUND.  
PI Glomski CA, Gong JK;  
DR WPI: 97-259141/23.  
PT Detecting exposure to radiation or radio-mimetic agents - by  
PT correlating with a protein, such as transferrin receptor, present on  
PT the surface of red blood cells of a mammal  
PS Disclosure; Page 61-62; 83pp; English.  
CC This polypeptide comprises the rat transferrin receptor (TR).  
CC claimed methods for detecting a mammal's prior exposure to  
CC radiation or radiomimetic agents (RAS) involve: isolating red blood  
CC cells from the mammal, and detecting the quantity of TRs on the red  
CC blood cells using e.g. an antibody raised against the TR. The  
CC quantity of TRs on the red blood cells is correlated with the  
CC mammal's prior exposure. It is possible to assess accurately  
CC low doses of radiation, e.g. on cancer risk and other delayed  
CC responses. The limited amount of blood necessary permits the test  
CC to be conducted as frequently as desired. The test's sensitivity,  
CC extending from 0.1 cGy to over 600 cGy, spans both the environmental  
CC and the lethal dose ranges.  
SQ Sequence 622 AA;

Query Match 77.4%: Score 48; DB 24; Length 622;  
Best Local Similarity 57.1%: Pred. No. 4.00e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 498 g1slqwl 504  
|:::|  
QY 50 GINLHML 56

RESULT 8  
ID W22213 standard; Protein: 760 AA.  
AC W22213:  
DT 02-NOV-1997 (first entry)  
DE Human transferrin receptor.  
KW Radiation; radiomimetic; exposure; transferrin receptor;  
KW red blood cell; human.  
OS Homo sapiens.  
PN W09715830-A1.  
PD 01-MAY-1997.  
PF 21-OCT-1996; U16880.  
PR 24-OCT-1995; US-547197.  
PA (UNYNY) UNIV NEW YORK STATE RES FOUND.  
PI Glomski CA, Gong JK;  
DR WPI: 97-259141/23.  
PT Detecting exposure to radiation or radio-mimetic agents - by  
PT correlating with a protein, such as transferrin receptor, present on  
PT the surface of red blood cells of a mammal  
PS Disclosure; Page 63-65; 83pp; English.  
CC This polypeptide comprises the human transferrin receptor (TR).  
CC claimed methods for detecting a mammal's prior exposure to  
CC radiation or radiomimetic agents (RAS) involve: Isolating red blood  
CC cells from the mammal, and detecting the quantity of TRs on the red  
CC blood cells using e.g. an antibody raised against the TR. The  
CC quantity of TRs on the red blood cells is correlated with the  
CC mammal's prior exposure. It is possible to assess accurately  
CC cumulative lifetime exposure and to directly study the effects of

CC low doses of radiation, e.g. on cancer-risk and other delayed  
 CC responses. The limited amount of blood necessary permits the test  
 CC to be conducted as frequently as desired. The test's sensitivity,  
 CC extending from 0.1 cGy to over 600 cGy, spans both the environmental  
 CC and the lethal dose ranges.  
 SQ Sequence 760 AA;

Query Match 77.4%; Score 48; DB 24; Length 760;  
 Best Local Similarity 57.1%; Pred. No. 4.00e+02;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 636 g1slqwl 642  
 1:1:1:1  
 OY 50 GINLHML 56

RESULT 9  
 ID P81342 standard; protein; 321 AA.  
 DE P81342;  
 19-OCT-1990 (first entry)  
 DE Polypeptide involved in protective mechanisms  
 KW Immune response; cell growth.  
 KM J63032898-A.  
 PD 30-JAN-1988.  
 PE 16-JUL-1986; 167518.  
 PR 16-JUL-1986; JP-167518.  
 PA (DAIN) Daiinpon Pharm KK.  
 DR WPI: 88-068419/10.  
 DE P-PSDB: P81312.  
 PT New polypeptide and DNA encoding it - related to protective  
 PS mechanisms such as immune response etc.  
 CC Disclosure: P; Japanese.  
 CC This polypeptide is involved in protective mechanisms such as immune  
 CC response, cell growth and activation of protective functions.  
 SQ Sequence 321 AA;

Query Match 74.2%; Score 46; DB 1; Length 321;  
 Best Local Similarity 57.1%; Pred. No. 5.83e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 133 gvdlaql 139  
 1:1:1:1  
 OY 50 GINLHML 56

RESULT 10  
 ID R04066 standard; protein; 356 AA.  
 DE R04066;  
 03-SEP-1990 (first entry)  
 DE T-variabilis D-amino acid oxidase gene product.  
 KW D-amino acid oxidase; cephalosporin; cephem; E.coli.  
 OS Trigonopsis variabilis.  
 PN EP-364275-A.  
 PD 18-APR-1990.  
 PE 12-OCT-1989; 310483.  
 PR 13-OCT-1988; JP-260332.  
 PA (FUJI) Fujisawa Pharm KK.  
 PI Isogai T, Ono H, Kojo H;  
 DR WPI: 90-11777/16.  
 DE D-amino acid oxidase, prodn.  
 PT by culture of E.coli transformants contg. expression vectors  
 PT originated from Fusarium solani M-0718.  
 PS Disclosure: Fig 9; 38pp; English.  
 CC E.coli transformed to express DAO, which catalyses the enzymatic  
 CC conversion of cephalosporin C to 7-beta-(5-carboxy-5-oxopentanamido)cephalosporanic acid (keto-7ACA). 7ACA is an  
 CC important starting point for the production of cephem  
 CC antibiotics.  
 SQ Sequence 356 AA;

Query Match 74.2%; Score 46; DB 3; Length 356;  
 Best Local Similarity 57.1%; Pred. No. 5.83e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 149 gyylnwl 155  
 1:1:1:1  
 OY 50 GINLHML 56

RESULT 11  
 ID P70388 standard; protein; 356 AA.  
 DE P70388;  
 14-JAN-1991 (first entry)  
 DE D-amino acid oxidase.  
 KW D-amino acid oxidase; Trigonopsis variabilis; cephalosporin;  
 OS Trigonopsis variabilis.  
 PN J62262994-A.  
 PD 16-NOV-1987.  
 PE 12-MAY-1986; J06663.  
 PR 12-MAY-1986; JP-106663.  
 PA (ASAHI) ASAHI CHEMICAL IND KK.  
 DR WPI: 87-359677/51.  
 DE N-PSDB: N70609.  
 PT DNA fragment encoding D-amino acid oxidase - which is a useful  
 PT enzyme for the catalytic oxidative deamination of D-amino acids.  
 PS Claim 1; page 583-4; 12pp; Japanese.  
 CC D-amino acid oxidase catalyses the oxidative deamination of D-amino  
 CC acids. It is used in the sepn. of L-amino acids from racemates,  
 CC in the prepn. of ketoic acid from D-amino acid, in amino acid  
 CC analysis, etc. The enzyme can oxidise cephalosporin C to  
 CC 7-beta-(5-carboxy-5-oxopentanamido)cephalosporanic acid, which  
 CC reacts with hydrogen peroxide to give 7-beta-(4-carboxybutanamido)-  
 CC cephalosporanic acid. These cpds. are important intermediates for  
 CC synthesis of cephalosporin type antibiotics.  
 SQ Sequence 356 AA;

Query Match 74.2%; Score 46; DB 2; Length 356;  
 Best Local Similarity 57.1%; Pred. No. 5.83e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 149 gyylnwl 155  
 1:1:1:1  
 OY 50 GINLHML 56

RESULT 12  
 ID R40916 standard; protein; 593 AA.  
 AC R40916;  
 DT 05-FEB-1994 (first entry)

DE Sequence of a CD26 fragment lacking a portion of the carboxy  
 DE terminal region  
 KW Human T cell activation antigen; monoclonal antibody T4; CD26.  
 OS Synthetic.  
 PN W09316102-A.  
 PD 19-AUG-1993.  
 PE 09-APR-1992; U02892.  
 PR 06-FEB-1992; US-832211.  
 PA (DAND) DANA FARMER CANCER INST INC.  
 PI Morimoto C, Schlossman SF, Tanaka T;  
 DR WPI: 93-272827/34.  
 DE Polypeptide fragments of CD26 - are capable of disrupting binding  
 PT of CD45 and CD26 and thus interfering with T-cell activation  
 PT Example: Pages 46-48; 73pp; English.  
 CC C26 is a human T cell activation antigen originally identified by  
 CC its reactivity with the Mab T41. C26 cDNA library was constructed  
 CC from human pHA-activated T cells using the CDM7 vector.  
 CC Fragments of CD26 can be prep'd in the following manner.  
 CC CD26 XbaI-SphI cDNA fragment is ligated to the vector.  
 CC RCSR-alpha-26 XbaI-HindIII DNA fragment and the linker Q46092.  
 CC The linker introduces an in-frame stop codon that results in the  
 CC deletion of the segment of CD26 from AA 594 to the carboxy  
 CC terminus of the wild-type protein. This deletion mutant, shown  
 CC in R40916, lacks the putative catalytic site of CD26 and has a new  
 CC carboxy terminus given in R40917.  
 SQ Sequence 593 AA;

Query Match 74.2% Score 46; DB 8; Length 593;  
 Best Local Similarity 66.7%; Pred. No. 5.83e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 311 Islql 316  
 111111  
 OY 51 INLHML 56

RESULT 13  
 ID R34614 standard; Protein; 593 AA.  
 AC R34614;  
 DT 09-DEC-1994 (first entry)  
 DE Delta594-C CD26  
 KW Human; T cell activation antigen; CD26; analogues: deletion; soluble;  
 KW signal peptidase; immune-stimulating; response-stimulating; AIDS;  
 KW immunosuppression; AIDS-related complex.  
 OS Homo sapiens.  
 PS Key Location/Qualifiers  
 misc\_difference 593  
 /note- "Position of delta594-C deletion"

PI W09409132-A.  
 PN 28-APR-1994.  
 PD 19-AUG-1993; U07923.  
 PR 21-AUG-1992; US-934162.  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PI Morimoto C, Schlossman S, Tanaka T;  
 DR WPI; 94-151317/18.  
 PT Polypeptide fragments and analogues of CD26 and encoding nucleic acid - useful for stimulating immune response, e.g. for treatment of AIDS to counteract immunosuppressive drug, and as vaccine adjuvant.  
 PS Disclosure; Page 56-58; 85pp; English.  
 CC The sequences given in R34612-14 represents analogues of the human T cell activation antigen CD26 which have internal deletions. The analogues pref. lack residues 3-9 or 24-34. These analogues are soluble under physiological conditions and lack enough amino acid residues to render them susceptible to cleavage by signal peptidase. CC The peptide fragments and analogues are useful as immune or response-stimulating therapeutics, eg. they may be used for treatment of disease conditions characterised by immunosuppression, eg. AIDS or AIDS-related complex, other virally or environmentally-induced conditions, and certain congenital immune deficiencies. The peptides can be employed to increase immune function which has been impaired by use of immunosuppressive drugs, such as certain chemotherapeutic drugs. CC Sequence 593 AA;

Query Match 74.2% Score 46; DB 10; Length 593;  
 Best Local Similarity 66.7%; Pred. No. 5.83e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 311 Islql 316  
 111111  
 OY 51 INLHML 56

RESULT 14  
 ID W34411 standard; Protein; 642 AA.  
 AC W34411;  
 DT 08-JUN-1998 (first entry)  
 DE Yeast acyl-coenzyme A:cholesterol acyltransferase-related enzyme II.  
 AC Acyl-coenzyme A:cholesterol acyltransferase; ACAT II;  
 KW ACAT related gene product I; ARGP-1; ARP-2; sterol esterification;  
 KW inhibitor; atherosclerosis; hyperlipidaemia; yeast.  
 OS Saccharomyces cerevisiae.  
 PS Key Location/Qualifiers  
 FT Domain 215..231  
 /note- "transmembrane domain"  
 FT Domain 439..451  
 /note- "transmembrane domain"  
 PN W09745439-A1.  
 PD 04-DEC-1997.

30-MAY-1997; U09460.  
 PR 30-MAY-1996; US-657620.  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 PI Sturley SL;  
 DR WPI; 98-032573/03.  
 DR N-PSDB; V01538.  
 PT DNA encoding acyl-coenzyme A: cholesterol acyltransferase II or PT II - useful to identify inhibitors for treatment of atherosclerosis or hyperlipidaemia  
 PS Disclosure; Fig 5C 1-3; 11pp; English.  
 CC This protein comprises yeast acyl-coenzyme A:cholesterol acyltransferase-related enzyme II. The invention relates to isolated nucleic acids (see V01533-35) coding for human and mouse acyl-coenzyme A:cholesterol acyltransferase II and III (see W34405-08), also designated ACAT related gene products (ARGP) 1 and 2. These can be used to identify inhibitors useful in the treatment of atherosclerosis and hyperlipidaemia.  
 CC Sequence 642 AA;

Query Match 74.2% Score 46; DB 29; Length 642;  
 Best Local Similarity 66.7%; Pred. No. 5.83e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 316 Iklnw1 321  
 111111  
 OY 51 INLHML 56

RESULT 15  
 ID W38418 standard; Protein; 642 AA.  
 AC W38418;  
 DT 21-MAY-1998 (first entry)  
 DE Yeast acyl-coenzyme A:cholesterol acyltransferase 2.  
 KW Acyl-coenzyme A:cholesterol acyltransferase 2; ARE2; yeast; sterol; esterification; arteriosclerosis; hyperlipidaemia;  
 KW antifungal; fungicide.  
 OS Saccharomyces cerevisiae.  
 PS Key Location/Qualifiers  
 FT Domain 215..231  
 /note- "putative transmembrane domain"  
 FT Domain 439..451  
 /note- "putative transmembrane domain"

PN W09745536-A1.  
 PD 04-DEC-1997.  
 PR 30-MAY-1997; U09160.  
 PR 30-MAY-1996; US-657621.  
 PA (INDV ) UNIV COLUMBIA NEW YORK.  
 PI (UYCO ) UNIV INDIANA FOUND.  
 PI Bard M, Sturley SL, Yang H;  
 DR WPI; 98-032644/03.  
 DR N-PSDB; T96370.  
 PT Yeast acyl-coenzyme A:cholesterol acyltransferase related enzyme I and II - useful to identify inhibitor for treatment of hyperlipidaemia, arteriosclerosis and fungal invasion  
 PS Example 1; Page 71-73; 11pp; English.  
 CC Yeast acyl-coenzyme A:cholesterol acyltransferase 2 (ARE2) is encoded by a gene (see T96370) located on chromosome X or XIV that was identified by homology to the human acyl-coenzyme A:cholesterol acyltransferase 1 gene (see T96368). ARE2 and ARE1 (see W38417) exhibit significant structural and functional homology to the putative catalytic component of cholesterol esterification in human macrophages. A consensus sequence of the yeast and human proteins is given in W38419. Deletion of the ARE1 and ARE2 genes produces a viable yeast cell with undetectable esterified sterol. CC A claimed expression vector comprises a nucleic acid molecule encoding yeast wild type ARE1 or ARE2 operatively linked to a promoter of RNA transcription. The vector and a claimed host-vector system can be used for the recombinant production of CC ARE1 or ARE2. The products can be used to identify novel ARE1 or CC ARE2 inhibitors. ARE2 inhibitors can be used to treat arteriosclerosis or hyperlipidaemia. ARE1 and ARE2 inhibitors can also be used to inhibit fungal growth or to treat fungal invasion (all claimed).

Sequence 642 AA;

Query Match

74.2%; Score 46; DB 28; Length 642;

Best Local Similarity 66.7%;

Pred. No. 5.83e+02;

Mismatches 0; Indels 0; Gaps 0;

Db 316 1k1hw1 321

OY 51 INLHWL 56

Search completed: Tue Apr 20 14:07:03 1999  
Job time : 16 secs.



ALTERNATE\_NAMES protein L1539; protein YLR006c  
ORGANISM #formal\_name Saccharomyces cerevisiae  
DATE 01-Aug-1995 #sequence\_revision 24 May-1996 #text\_change  
06-Feb-1998  
ACCESSIONS S64828; S45308  
REFERENCE S64742  
#authors Vandenbol, M.; Portetelle, D.; Hliger, F.  
#submission submitted to the Protein Sequence Database, May 1996  
#accession S64828  
#molecule\_type DNA  
#residues 1-712 #label VAN  
#cross-references EMBL:Z73178; NID:g1360295; PID:e245767; PID:g1360296;  
MIPS:YLR006c  
#experimental\_source strain S288C  
REFERENCE S45308  
#authors Maeda, T.; Wurgler-Murphy, S.M.; Saito, H.  
#journal Nature (1994) 369:242-245  
#title A two-component system that regulates an osmosensing MAP  
kinase cascade in yeast.  
#accession S45308  
#status nucleic acid sequence not shown; not compared with  
#molecule\_type DNA  
#residues 1-180,'S',182-712 #label MAE  
GENETICS #gene SGD:SSK1  
#cross-references SGD:S0003996; MIPS:YLR006c  
FUNCTION #map\_position 12R  
#description signal transduction  
CLASSIFICATION #superfamily response regulator homology  
KEYWORDS phosphoprotein; signal transduction; two-component regulatory  
system  
FEATURE  
506-613 #domain response regulator homology #label RRH\  
554 #binding-site phosphate (Asp) (covalent) #status  
predicted  
SUMMARY #length 712 #molecular\_weight 78529 #checksum 1343  
Query Match 85.5%; Score 53; DB 2; Length 712;  
Best Local Similarity 83.3%; Pred. No. 2.29e+01;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 634 VNLHML 639  
QY 51 INLHML 56  
RESULT 3  
ENTRY #type complete  
TITLE probable mmp14 protein - Mycobacterium tuberculosis (strain  
H37RV)  
ORGANISM #formal\_name Mycobacterium tuberculosis  
DATE 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change  
17-Jul-1998  
ACCESSIONS C70831  
REFERENCE A70500  
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,  
C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gao, S.; Barry  
III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.;  
Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;  
Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;  
Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;  
Murphy, L.; Oliver, S.; Osborn, J.; Quail, M.A.;  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;  
Skellton, S.; Squares, S.; Squires, R.; Sulston, J.E.;  
Taylor, K.; Whitehead, S.; Barrell, B.G.  
#journal Nature (1998) 393:537-544  
#title Deciphering the biology of Mycobacterium tuberculosis from  
the complete genome sequence.  
#cross-references M01D:98295987  
#accession C70831  
#status preliminary; nucleic acid sequence not shown;

translation not shown  
#molecule\_type DNA  
#residues 1-967 #label COL  
#cross-references GB:AL021932; GB:AL123456; NID:g93261527; PID:e1252519;  
PID:g2909525  
#experimental\_source strain H37RV  
GENETICS #gene mmp14  
SUMMARY #length 967 #molecular\_weight 105233 #checksum 3274  
Query Match 85.5%; Score 53; DB 2; Length 967;  
Best Local Similarity 71.4%; Pred. No. 2.29e+01;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Db 823 AILHML 829  
QY 50 GINLHML 56  
RESULT 4  
ENTRY #type complete  
TITLE NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 -  
chicken mitochondrion (SGC1)  
ORGANISM #formal\_name mitochondrion Gallus gallus #common\_name chicken  
DATE 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change  
08-Sep-1997.  
ACCESSIONS S10196  
REFERENCE S10187  
#authors Desjardins, P.; Morris, R.  
#journal J. Mol. Biol. (1990) 212:599-634  
#title Sequence and gene organization of the chicken mitochondrial  
genome. A novel gene order in higher vertebrates.  
#cross-references M01D:90230301  
#accession S10196  
#molecule\_type DNA  
#residues 1-459 #label DES  
#cross-references EMBL:X52392; NID:g12360; PID:g12970  
GENETICS #gene ND4  
#genome mitochondrion  
#genetic\_code SGC1  
CLASSIFICATION #superfamily NADH dehydrogenase (ubiquinone) chain 4  
KEYWORDS membrane-associated complex; mitochondrion; NAD; oxidative  
phosphorylation; oxidoreductase; respiratory chain  
SUMMARY #length 459 #molecular\_weight 51145 #checksum 1806  
Query Match 83.9%; Score 52; DB 2; Length 459;  
Best Local Similarity 71.4%; Pred. No. 3.25e+01;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Db 36 SISLHML 42  
QY 50 GINLHML 56  
RESULT 5  
ENTRY #type complete  
TITLE hypothetical protein - Synecocystis sp. (strain PCC 6803)  
ORGANISM #formal\_name Synecocystis sp.  
#varley PCC 6803  
DATE 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change  
21-Aug-1998  
ACCESSIONS S75895  
REFERENCE S74322  
#authors Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;  
Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugitara, M.;  
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;  
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimo,  
S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;  
Yasuda, M.; Tabata, S.  
#journal DNA Res. (1996) 3:109-136  
#title Sequence analysis of the genome of the unicellular  
cyanobacterium Synecocystis sp. PCC6803. II. Sequence



determination of the entire genome and assignment of potential protein-coding regions.

#cross-references MUID:97061201

#accession S75895

#status preliminary

#molecule\_type DNA

#residues 1-495 ##label KAN

#cross-references EMBL:D90913; GB:AB001339; NID:g1653348; PID:d1019087;

PID:g1653440

##note the nucleotide sequence was submitted to the EMBL Data

Library, June 1996

CLASSIFICATION #superfamily xylinokinase

SUMMARY #length 495 #molecular-weight 54351 #checksum 4379

Query Match 82.3%; Score 51; DB 2; Length 495;

Best Local Similarity 71.4%; Pred. No. 4.60e+01;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 141 GINLHML 147

50 GINLHML 56

RESULT 6

ENTRY #type complete

TITLE Probable tRNA delta(2)-isopentenylpyrophosphate transferase

ORGANISM #formal\_name Treponema pallidum subsp. pallidum #common\_name

sypillis spirochete

DATE 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change

07-Aug-1998

ACCESSIONS

REFERENCE B71301

#authors

Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.;

Sutton, G.G.; Dodson, R.; Gwin, M.; Hickey, E.K.; Clayton,

R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod,

M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson,

D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McDonald,

L.; Artlisch, P.; Bowman, C.; Cotton, M.D.; Fujii, C.;

Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Matthey,

L.; Weidman, J.; Smith, H.O.; Venter, J.C.

#journal Science (1998) 281:375-388

#title Complete genome sequence of Treponema pallidum, the sypillis

spirochete.

#accession B71301

#status preliminary; nucleic acid sequence not shown;

translation not shown

#molecule\_type DNA

#residues 1-316 ##label COL

#cross-references GB:AE001238; GB:AE000520; NID:g3322928; PID:g3322935

#experimental\_source strain Nichols

GENETICS

#gene

SUMMARY #length 316 #molecular-weight 36174 #checksum 2660

Query Match 80.6%; Score 50; DB 2; Length 316;

Best Local Similarity 57.1%; Pred. No. 6.47e+01;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 300 GVKIHWL 306

50 GINLHML 56

RESULT 7

ENTRY #type complete

TITLE B70661 #type complete, hypothetical protein RV2337c - Mycobacterium tuberculosis

ORGANISM (strain H37RV)

DATE #formal\_name Mycobacterium tuberculosis

17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change

ACCESSIONS

REFERENCE B70661

A70500

#authors

Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,

C.; Harris, D.; Gordon, S.V.; Eigemeier, K.; Gas, S.; Barry

III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.;

Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;

Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;

Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;

Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;

Rajadream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;

Skellton, S.; Squares, S.; Squires, R.; Sulston, J.E.;

Taylor, K.; Whitehead, S.; Barrall, B.G.

#journal Nature (1998) 393:537-544

#title Deciphering the biology of Mycobacterium tuberculosis from

the complete genome sequence.

#cross-references MUID:98295987

#accession B70661

#status preliminary; nucleic acid sequence not shown;

translation not shown

#molecule\_type DNA

#residues 1-372 ##label COL

#cross-references GB:Z83860; GB:AL123456; NID:g3261681; PID:e290744;

PID:g1781244

#experimental\_source strain H37RV

GENETICS

#gene

SUMMARY #length 372 #molecular-weight 41272 #checksum 8278

Query Match 80.6%; Score 50; DB 2; Length 372;

Best Local Similarity 71.4%; Pred. No. 6.47e+01;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 154 GJOLHWF 160

50 GINLHML 56

RESULT 8

ENTRY #type complete

TITLE A70477 #type complete

ORGANISM #formal\_name Aquifex aeolicus

DATE 08-May-1998 #sequence\_revision 08-May-1998 #text\_change

13-Sep-1998

ACCESSIONS

REFERENCE A70477

#authors

Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;

Lenox, A.L.; Graham, D.E.; Overbeek, R.; Sneed, M.A.;

Keller, M.; AuJay, M.; Huber, R.; Feldman, R.A.; Short,

J.M.; Olson, G.J.; Swanson, R.V.

#journal Nature (1998) 392:353-358

#title The complete genome of the hyperthermophilic bacterium

Aquifex aeolicus.

#cross-references MUID:98196666

#accession A70477

#status preliminary; nucleic acid sequence not shown;

translation not shown

#molecule\_type DNA

#residues 1-476 ##label AOF

#cross-references GB:AE000770; NID:g2984274; PID:g2984275; GB:AE000657

#experimental\_source strain VFS

GENETICS

#gene

CLASSIFICATION #superfamily glutamate synthase small chain

SUMMARY #length 476 #molecular-weight 52947 #checksum 4062

Query Match 80.6%; Score 50; DB 2; Length 476;

Best Local Similarity 57.1%; Pred. No. 6.47e+01;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 342 GVKIHWL 348

50 GINLHML 56

RESULT 9

ENTRY #type complete

TITLE B70661 #type complete, hypothetical protein RV2337c - Mycobacterium tuberculosis

ORGANISM (strain H37RV)

DATE #formal\_name Mycobacterium tuberculosis

17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change

ACCESSIONS

REFERENCE B70661

A70500

ENTRY B64126 #type complete  
TITLE transposase homolog H1478 - Haemophilus influenzae (strain Rd KW20)  
ORGANISM #formal\_name Haemophilus influenzae  
DATE 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997  
ACCESSIONS B64126  
REFERENCE A64000  
#authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Heblum, E.; Cotton, M.D.; Uterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrman, J.L.; Geoghegan, N.S.M.; Gnehm, C.L.; McDonald, J.L.; Small, R.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.  
#journal Science (1995) 269:496-512  
#title Whole-genome random sequencing and assembly of Haemophilus influenzae Rd  
#cross-references M01D:95350630  
#accession B64126  
#status nucleic acid sequence not shown; translation not shown  
#molecule\_type DNA  
#residues 1-687 ##label TIGR  
#cross-references GB:U32825; GB:L42023; NID:g1574307; PID:g1574318; TIGR:H1478  
SUMMARY #length 687 #molecular-weight 78719 #checksum 2570  
Query Match 80.6%; Score 50; DB 2; Length 687;  
Best Local Similarity 83.3%; Pred. No. 6.47e+01;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 379 GINLHW 384  
OY 50 GINLHW 55  
RESULT 10  
ENTRY D64629 #type complete  
TITLE iron-regulated outer membrane protein - Helicobacter pylori (strain 26695)  
ORGANISM #formal\_name Helicobacter pylori  
DATE 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 18-Sep-1998  
ACCESSIONS D64629  
REFERENCE A64520  
#authors Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klein, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalaki, H.G.; Glodek, A.; McKenney, K.; Fitzgerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Uterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney, L.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.  
#journal Nature (1997) 388:539-547  
#title The complete genome sequence of the gastric pathogen Helicobacter pylori.  
#cross-references M01D:97394467  
#accession D64629  
#status preliminary; nucleic acid sequence not shown; translation not shown  
#molecule\_type DNA  
#residues 1-791 ##label TOM  
#cross-references GB:AE000597; GB:AE000511; NID:92314007; PID:92314011; TIGR:HP0876  
CLASSIFICATION #superfamily iron-regulated outer membrane protein  
SUMMARY #length 791 #molecular-weight 88525 #checksum 366

Query Match 80.6%; Score 50; DB 2; Length 791;  
Best Local Similarity 85.7%; Pred. No. 6.47e+01;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
DB 665 GINLHW 671  
OY 50 GINLHW 56  
RESULT 11  
ENTRY S04085 #type complete  
TITLE ovarian tumor locus protein - fruit fly (Drosophila melanogaster)  
ORGANISM #formal\_name Drosophila melanogaster  
DATE 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 24-Sep-1998  
ACCESSIONS S04085  
REFERENCE S04085  
#authors Champe, M.A.; Laird, C.D.  
#journal Nucleic Acids Res. (1989) 17:3304  
#title Nucleotide sequence of a cDNA from the putative ovarian tumor locus of Drosophila-melanogaster.  
#cross-references M01D:89263747  
#accession S04085  
#status translation not shown  
#molecule\_type mRNA  
#residues 1-811 ##label CHA  
#cross-references EMBL:X13693; NID:98315; PID:98316  
GENETICS  
#gene otu  
#cross-references FlyBase:FBgn0003023  
SUMMARY #map\_position X #length 811 #molecular-weight 92616 #checksum 7288  
Query Match 80.6%; Score 50; DB 2; Length 811;  
Best Local Similarity 66.7%; Pred. No. 6.47e+01;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
DB 593 GVDLHW 598  
OY 50 GINLHW 55  
RESULT 12  
ENTRY A33829 #type complete  
TITLE ovarian tumor protein - fruit fly (Drosophila melanogaster)  
ORGANISM #formal\_name Drosophila melanogaster  
DATE 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 24-Sep-1998  
ACCESSIONS A33829  
REFERENCE A33829  
#authors Steinhauser, W.R.; Walsh, R.C.; Kalfayan, L.J.  
#journal Mol. Cell. Biol. (1989) 9:5726-5732  
#title Sequence and structure of the Drosophila melanogaster ovarian tumor gene and generation of an antibody specific for the ovarian tumor protein.  
#cross-references M01D:9006528  
#accession A33829  
#status preliminary  
#molecule\_type DNA; mRNA  
#residues 1-811 ##label STR  
#cross-references GB:M30825; NID:g158028; PID:g158029  
GENETICS  
#gene FlyBase:otu  
#cross-references FlyBase:FBgn0003023  
SUMMARY #length 811 #molecular-weight 92612 #checksum 7006  
Query Match 80.6%; Score 50; DB 2; Length 811;  
Best Local Similarity 66.7%; Pred. No. 6.47e+01;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
DB 593 GVDLHW 598  
OY 50 GVDLHW 598

QY 50 GINLHML 55

RESULT 13

ENTRY 138150 #type complete

ORGANISM Rb2/p130 protein - human

DATE 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 29-Aug-1997

ACCESSIONS 138150; S36648

REFERENCE 138150

#authors Mayol, X.; Grana, X.; Baldi, A.; Sang, N.; Hu, Q.; Giordano, A.

#journal Oncogene (1993) 8:2561-2566

#title Cloning of a new member of the retinoblastoma gene family (pRb2) which binds to the E1A transforming domain.

#cross-references MUID:93368960

#accession 138150

#status Preliminary; translated from GB/EMBL/DBJ

#molecule\_type mRNA

##residues 1-1082 ##label RES

##cross-references EMBL:X74594; NID:9397147; PID:9397148

GENETICS

#gene GDB:RBL2

##cross-references GDB:269890; OMIM:180203

#map\_position 16q12.2-16q12.2

CLASSIFICATION #superfamily retinoblastoma-associated protein

SUMMARY #length 1082 #molecular\_weight 122475 #checksum 2127

Query Match 80.6%; Score 50; DB 2; Length 1082;

Best Local Similarity 71.4%; Pred. NO. 6.47e+01;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 24 GNDLHML 30

QY 50 GINLHML 56

RESULT 14

ENTRY A49370 #type complete.

TITLE E1A-associated cyclin-binding protein p130 - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Mar-1998

ACCESSIONS A49370

REFERENCE A49370

#authors Hannon, G.J.; Demetrick, D.; Beach, D.

#journal Genes Dev. (1993) 7:2378-2391

#title Isolation of the Rb-related p130 through its interaction with CDK2 and cyclins.

#cross-references MUID:94074896

#accession A49370

#status Preliminary

#molecule\_type mRNA

##residues 1-1139 ##label HAN

##cross-references GB:S67171; NID:9453131; PID:9453132

##experimental\_source HeLa S3 suspension cells

##note sequence extracted from NCBI backbone (NCBIN:140576, NCBIP:140577)

CLASSIFICATION #superfamily retinoblastoma-associated protein

SUMMARY #length 1139 #molecular\_weight 128366 #checksum 5271

Query Match 80.6%; Score 50; DB 2; Length 1139;

Best Local Similarity 71.4%; Pred. NO. 6.47e+01;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 81 GNDLHML 87

QY 50 GINLHML 56

RESULT 15

ENTRY A49369 #type complete.

TITLE adenovirus E1A-associated 130k protein - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 03-May-1996

ACCESSIONS A49369

REFERENCE A49369

#authors Li, Y.; Graham, C.; Lacy, S.; Duncan, A.M.V.; Whyte, P.

#journal Genes Dev. (1993) 7:2366-2377

#title The adenovirus E1A-associated 130-kD protein is encoded by a member of the retinoblastoma gene family and physically interacts with cyclins A and E.

#accession A49369

#status Preliminary

#molecule\_type mRNA

##residues 1-1139 ##label LIA

##cross-references GB:X76061

CLASSIFICATION #superfamily retinoblastoma-associated protein

SUMMARY #length 1139 #molecular\_weight 128451 #checksum 5554

Query Match 80.6%; Score 50; DB 2; Length 1139;

Best Local Similarity 71.4%; Pred. NO. 6.47e+01;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 81 GNDLHML 87

QY 50 GINLHML 56

Search completed: Tue Apr 20 14:06:29 1999

Job time : 19 secs.

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RESULT 2  
ID YDK9.SCHPO STANDARD: PRT: 1033 AA.  
AC P87115;  
DT 15-JUL-1998 (REL. 36, CREATED)  
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)  
DE HYPOTHETICAL 116.5 KD PROTEIN C2068.09C IN CHROMOSOME I.  
GN SPAC2068.09C  
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-972;  
RA BADCOCK K., CHURCHER C.M., WOOD V., BARRELL B.G., RAJANDEAN M.A.;  
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -1- SIMILARITY: TO YEAST YNL132W AND AN A.AMBISEXUALIS HYPOTHETICAL  
PROTEIN (AC P54008).  
EMBL: 295334; E315494;  
HYPOTHETICAL PROTEIN: ATP-BINDING.  
NP BIND 282  
SQ SEQUENCE 1033 AA; 116463 MW; ACDA931 CRC32;  
Query Match 85.5%; Score 53; DB 1; Length 1033;  
Best Local Similarity 83.3%; Pred. No. 7.08e+00;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 38 VNLHWL 43  
QY 51 INLHWL 56

RESULT 3  
ID N14M.CHICK STANDARD: PRT: 459 AA.  
AC P18939;  
DT 01-NOV-1990 (REL. 16, CREATED)  
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)  
DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).  
GN MTNDA OR NDA OR NADH4.  
OS GALLUS GALLUS (CHICKEN).  
OC MITOCHONDRION.  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;  
OC GALLIFORMES.  
RN [1]  
RP SEQUENCE FROM N.A.  
MEDLINE: 90230301.  
CC DESJARDINS P., MORAIS R.;  
J. MOL. BIOL. 212:599-634(1990).  
-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.  
DR EMBL: X52392; G12970;  
PIR: S10196; S10196.  
KM OXIDOREDUCTASE, NAD; UBIQUINONE; MITOCHONDRION.  
SQ SEQUENCE 459 AA; 51145 MW; 88198353 CRC32;  
Query Match 83.9%; Score 52; DB 1; Length 459;  
Best Local Similarity 71.4%; Pred. No. 1.05e+01;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 36 SISLHWL 42  
QY 50 GINLHWL 56

RESULT 4  
ID GLPK-STYNS STANDARD: PRT: 495 AA.  
AC P74260;  
DT 01-NOV-1997 (REL. 35, CREATED)  
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
DE GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE)  
GN GLPK OR SLR1672.

OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).  
OC PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;  
OC CYANOBACTERIA (BLUE-GREEN ALGAE); CHROCOCCALES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 97061201.  
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,  
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASANOTO S., KIMURA T.,  
RA HOSOTUCHI T., MATSUNO A., MORI A., NAKAZAKI N., NARDO K.,  
RA OKUMURA S., SHIMO S., TAKEUCHI C., WADA T., WATANABE A.,  
RA YAMADA M., YASUDA M., TABATA S.;  
RL DNA RES. 3:109-136(1996).  
CC -1- CATALYTIC ACTIVITY: ATP + GLYCEROL = ADP + GLYCEROL 3-PHOSPHATE.  
CC -1- PATHWAY: RATE-LIMITING STEP IN GLYCEROL UTILIZATION.  
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE FUCOKINASE / GLUCONOKINASE /  
GLYCEROKINASE / XYLOKINASE FAMILY.  
DR EMBL: D90913; G1653440;  
DR PROSITE: PS00933; FGGY\_KINASES\_1; FALSE\_NEG.  
DR PROSITE: PS00445; FGGY\_KINASES\_2; 1.  
KM GLYCEROL METABOLISM; TRANSFERASE; KINASE.  
SQ SEQUENCE 495 AA; 54351 MW; C7247592 CRC32;  
Query Match 82.3%; Score 51; DB 1; Length 495;  
Best Local Similarity 71.4%; Pred. No. 1.55e+01;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 141 GTRLHWL 147  
QY 50 GINLHWL 56

RESULT 5  
ID YFLM.CAEBL STANDARD: PRT: 1459 AA.  
AC Q21874;  
DT 15-JUL-1998 (REL. 36, CREATED)  
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)  
DE HYPOTHETICAL 166.0 KD PROTEIN R09E10.5 IN CHROMOSOME IV.  
GN R09E10.5.  
OS CAENORHABDITIS ELEGANS.  
OC EUKARYOTA; METAZOA; ACLOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.  
OC [1]  
RP SEQUENCE FROM N.A.  
RN STRAIN-BRISTOL N2;  
RA MATTHEWS L.;  
RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -1- SIMILARITY: STRONG, TO C.ELEGANS F54D1.6.  
DR EMBL: Z70287; E233847;  
KW WORMPEP; R09E10.5; CE06287.  
KM HYPOTHETICAL PROTEIN; TRANSMEMBRANE.  
SQ SEQUENCE 1459 AA; 165994 MW; 46E17445 CRC32;  
Query Match 82.3%; Score 51; DB 1; Length 1459;  
Best Local Similarity 83.3%; Pred. No. 1.55e+01;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 640 ISLHWL 645  
QY 51 INLHWL 56

RESULT 6  
ID OTU.DROME STANDARD: PRT: 811 AA.  
AC P10383;  
DT 01-MAR-1989 (REL. 10, CREATED)  
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)  
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)  
DE OVARIAN TUMOR LOCUS PROTEIN.  
GN OTU.  
OS DROSOPHILA MELANOGASTER (FRUIT FLY).  
OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.  
RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-CANTON-S;  
 RX MEDLINE: 89263747.  
 RA CHAMPE M.A., LAIRD C.D.;  
 RL NUCLEIC ACIDS RES. 17:3304-3304(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 90066528.  
 RA STEINHAUER W.R., WALSH R.C., KAUFMAN L.J.;  
 RL MOL. CELL. BIOL. 9:5726-5732(1989).  
 CC -1- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR FEMALE FERTILITY.  
 CC -1- SIMILARITY: LOW, WITH THE DROSOPHILA BAG-OF-MARBLE PROTEIN.  
 DR EMBL: X13693; G8316; -  
 DR EMBL: M30825; G158029; -  
 DR PIR: S04085; S04085.  
 DR PIR: A33829; A33829.  
 DR EMBL: F891003023; ctu.  
 FT CONFLICT 300  
 FT CONFLICT 789  
 Q -> K (IN REF. 2).  
 T -> P (IN REF. 2).  
 Q SEQUENCE 811 AA; 92616 MW; B8C8AC5D CRC32;

Query Match 80.6%; Score 50; DB 1; Length 811;  
 Best Local Similarity 66.7%; Pred. No. 2.29e+01;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 593 GVDLHW 598  
 QY 50 GINLHW 55

RESULT 7  
 ID RBL2 HUMAN STANDARD; PRT: 1082 AA.  
 AC C08999;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
 DE RETINOBLASTOMA-LIKE PROTEIN 2 (130 KD RETINOBLASTOMA-ASSOCIATED  
 DE PROTEIN) (P302) (P130).  
 GN RBL2 OR RB2  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUKARYOTA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93368960.  
 RA MAYOL X., GRANA X., BALDI A., SANG N., HU Q., GIORIANO A.;  
 RL ONCOGENE 8:2561-2566(1993).  
 CC -1- FUNCTION: MAY HAVE A FUNCTION IN CELL CYCLE REGULATION. BINDS TO  
 AND MAY BE INVOLVED IN THE TRANSFORMING CAPACITY OF THE ADENOVIRUS  
 E1A PROTEIN. MAY ACT AS A TUMOR SUPPRESSOR. POTENT INHIBITOR OF  
 E2F-MEDIATED TRANS-ACTIVATION. ASSOCIATES PREFERENTIALLY WITH  
 E2F5.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- SIMILARITY: BELONGS TO THE RETINOBLASTOMA PROTEIN (RB) FAMILY.  
 DR EMBL: X74594; G397148; -  
 DR MIM: 180203; -  
 KW TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN; CELL CYCLE;  
 KW PHOSPHORYLATION; ANTI-ONCOGENE.  
 FT DOMAIN 360 967  
 FT DOMAIN 360 559  
 FT DOMAIN 560 770  
 FT DOMAIN 771 967  
 FT DOMAIN 771 967  
 Q SEQUENCE 1082 AA; 122476 MW; 4F714A55 CRC32;

Query Match 80.6%; Score 50; DB 1; Length 1082;  
 Best Local Similarity 71.4%; Pred. No. 2.29e+01;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 24 GNDLHWL 30  
 QY 50 GINLHWL 56

RESULT 8  
 ID RPCL\_BP186 STANDARD; PRT: 192 AA.  
 AC P08707;  
 DT 01-JAN-1988 (REL. 06, CREATED)  
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE REPRESSOR PROTEIN CI.  
 GN CI.  
 OS BACTERIOPHAGE 186.  
 CC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; MYOVIRIDAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-186CIRSP;  
 RX MEDLINE: 87112711.  
 RA KALONIS B., DODD I.B., EGAN J.B.;  
 RL J. MOL. BIOL. 191:199-209(1986).  
 CC -1- FUNCTION: REPRESSOR OF LYSOGENY.  
 CC -1- SIMILARITY: TO PHAGE HPI CI AND TO ORF1 OF E. COLI RETRON EC67.  
 DR EMBL: X04449; G15554; -  
 DR PIR: S09533; S09533.  
 KW TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING.  
 Q SEQUENCE 192 AA; 21256 MW; 7D8E003E CRC32;

Query Match 79.0%; Score 49; DB 1; Length 192;  
 Best Local Similarity 71.4%; Pred. No. 3.34e+01;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 62 GANLHWL 68  
 QY 50 GINLHWL 56

RESULT 9  
 ID YNO2\_PARDE STANDARD; PRT: 214 AA.  
 AC P29908;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 22.9 KD PROTEIN IN N002 3' REGION (UNR2).  
 GN PARACOCUS DENTRIFICANS.  
 OS PARACOCUS DENTRIFICANS.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;  
 OC UNCERTAIN.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 13548;  
 RX MEDLINE: 91363357.  
 RA XU X., MATSUNO-YAGI A., YAGI T.;  
 RL BIOCHEMISTRY 30:8678-8684(1991).  
 CC -1- FUNCTION: URE2 PRODUCT MAY BE INVOLVED IN THE TRANSFER OF IRON-  
 SULFUR CLUSTERS TO THE NADH DEHYDROGENASE COMPLEX. IT MAY ALSO  
 BE REQUIRED FOR THE ASSEMBLY OF THE NADH DEHYDROGENASE COMPLEX.  
 CC -1- SIMILARITY: SIGNIFICANT TO ORF3 OF P. DENTRIFICANS (LOCATED  
 BETWEEN THE COX1 & COX11 GENES).  
 DR EMBL: M74171; G150604; -  
 DR PIR: B40296; B40296.  
 KW HYPOTHETICAL PROTEIN.  
 Q SEQUENCE 214 AA; 22906 MW; DA6A9F8A CRC32;

Query Match 79.0%; Score 49; DB 1; Length 214;  
 Best Local Similarity 75.0%; Pred. No. 3.34e+01;  
 Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Db 27 GIGDLHWL 34  
 QY 50 GINLHWL 56

RESULT 10  
 ID YD89\_SCHPO STANDARD; PRT: 561 AA.  
 AC Q10414;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN-CHROMOSOME I.  
 GN SPAC1F3.09.  
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
 OC EUKARYOTA: FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972:  
 RA CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;  
 RL SUBMITTED (APR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 CC -1- SIMILARITY: TO YEAST YGR093W.  
 DR EMBL: 270690; E234475; -  
 KM HYPOTHETICAL PROTEIN.  
 SQ SEQUENCE 561 AA; 63216 MW; EB2F8868 CRC32;  
 Query Match 79.0%; Score 49; DB 1; Length 561;  
 Best Local Similarity 66.7%; Pred. No. 3.34e+01;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 447 GVHLHW 452  
 1:1111  
 QY 50 GINLHW 55

RESULT 11  
 ID OPB\_ECOLI STANDARD; PRT: 306 AA.  
 AC P31132; P76026; P77550;  
 DT 01-JUL-1993 (REL. 26, CREATED)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DE OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPB.  
 GN OPB.  
 OS ESCHERICHIA COLI.  
 OC PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 CC ENTEROBACTERIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RA BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;  
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RA AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,  
 RA IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,  
 RA KASHIMOTO K., KIM S., KIMURA S., KITAGAWA M., KITAGAWA M., MAKINO K.,  
 RA MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y.,  
 RA NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,  
 RA TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.;  
 RA SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [3]  
 RP SEQUENCE OF 1-16 FROM N.A.  
 RC MEDLINE: 90256748.  
 RA KASHIMOTO K., YAMAGUCHI Y., SAKAI Y., KOBAYASHI H., IGARASHI K.;  
 RL J. BIOL. CHEM. 265:8387-8391(1990).  
 CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM  
 FOR OLIGOPEPTIDES; PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF  
 THE SUBSTRATE ACROSS THE MEMBRANE.  
 CC -1- SUBCELLULAR LOCATION: INTERAL MEMBRANE PROTEIN. INNER MEMBRANE.  
 CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-  
 PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPBEC  
 SUBFAMILY.  
 CC EMBL: AE000223; G1787497; -  
 DR EMBL: D90763; G1742033; -  
 DR EMBL: D90852; D1016767; -  
 DR EMBL: J05433; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: B36263; B36263.  
 DR ECOGENE: EG10675; OPB.  
 DR PROSITE: PS00402; BPD\_TRANSF. INN MEMBR. 1.  
 KM TRANSF. PEPTIDE TRANSPORT: TRANSMEMBRANE. INNER MEMBRANE.  
 FT DOMAIN 1 9 CYTOPLASMIC (PROBABLE).  
 FT TRANSMEM 10 30 PROBABLE.  
 FT TRANSMEM 31 99 EXTRACELLULAR (PROBABLE).  
 FT TRANSMEM 100 121 PROBABLE.

FT DOMAIN 122 137 CYTOPLASMIC (PROBABLE).  
 FT TRANSMEM 138 158 PROBABLE.  
 FT DOMAIN 159 172 EXTRACELLULAR (PROBABLE).  
 FT TRANSMEM 173 190 PROBABLE.  
 FT DOMAIN 191 226 CYTOPLASMIC (PROBABLE).  
 FT TRANSMEM 227 250 PROBABLE.  
 FT DOMAIN 251 271 EXTRACELLULAR (PROBABLE).  
 FT TRANSMEM 272 293 PROBABLE.  
 FT DOMAIN 294 306 CYTOPLASMIC (PROBABLE).  
 SQ SEQUENCE 306 AA; 33443 MW; 3FCC9F5 CRC32;  
 Query Match 77.4%; Score 48; DB 1; Length 306;  
 Best Local Similarity 71.4%; Pred. No. 4.87e+01;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Db 155 ALLHWL 161  
 1:1111  
 QY 50 GINLHW 56

RESULT 12  
 ID IPNS\_CEPAC STANDARD; PRT: 338 AA.  
 AC P05189;  
 DT 13-AUG-1987 (REL. 05, CREATED)  
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
 DE ISOPENICILLIN N SYNTHETASE (IPNS).  
 GN PCBC OR IPS.  
 OS CEPHALOSPORIUM ACREMONIUM (ACREMONIUM CHRYSOGENUM).  
 OC EUKARYOTA: FUNGI; ASCOMYCOTINA; PLEOTOMYCETES; EUROTIALES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE: 86040479.  
 RA SAMSON S.N., BELAGAJE R., BLANKENSHIP D.T., CHAPMAN J.L., PERRY D.,  
 RA SKATRUD P.L., VANFRANK R.M., ABRAHAM E.P., BALDWIN J.E., QUEENER S.W.,  
 RA INGOLIA T.D.;  
 RL NATURE 318:191-194(1985).  
 RN [2]  
 RP SEQUENCE OF 3-52.  
 RC STRAIN-ATCC 60777;  
 RX MEDLINE: 85285585.  
 RA BALDWIN J.E., GAGNON J., TING H.H.;  
 RL FEBS LETT. 188:253-256(1985).  
 RN [3]  
 RP SEQUENCE OF 40-78 AND 237-264, AND PHOTOAFFINITY LABELLING.  
 RA BALDWIN J.E., COATES J.B., MOLONEY M.G., PRATT A.J., WILDS A.C.;  
 RL BIOCHEM. J. 266:561-567(1990).  
 CC -1- CATALYTIC ACTIVITY: REMOVES, IN THE PRESENCE OF OXYGEN, 4 HYDROGEN  
 ATOMS FROM L-(ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE TO FORM THE  
 AZETIDINONE AND THIAZOLIDINE RINGS OF ISOPENICILLIN.  
 CC -1- COFACTOR: IRON AND ASCORBATE.  
 CC -1- PATHWAY: CENTRAL ROLE IN THE BIOSYNTHESIS OF PENICILLIN AND  
 CEPHALOSPORIN.  
 CC -1- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF  
 OXIDOREDUCTASES.  
 CC EMBL: X03148; G2506; -  
 DR PIR: A24567; A24567.  
 DR PIR: A23995; A23995.  
 DR PIR: S09312; S09312.  
 DR PROSITE: PS00185; IPNS\_1; 1.  
 DR PROSITE: PS00186; IPNS\_2; 1.  
 KM ANTI-BIOTIC BIOSYNTHESIS; OXIDOREDUCTASE; IRON; VITAMIN C.  
 FT CONFLICT 22 22 D -> T (IN REF. 2).  
 SQ SEQUENCE 338 AA; 38433 MW; EE264220 CRC32;  
 Query Match 77.4%; Score 48; DB 1; Length 338;  
 Best Local Similarity 57.1%; Pred. No. 4.87e+01;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Db 50 GVDPHWL 56  
 1:1111  
 QY 50 GINLHW 56



RESULT 13  
ID RPBE\_SALTI STANDARD; PRT; 338 AA.  
AC P14169;  
DT 01-JAN-1990 (REL. 13, CREATED)  
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE CDP-TYPELOSE-2-EPIMERASE (EC 5.1.3.-).  
GN RPBE.  
OS SALMONELLA TYPHI.  
OC PROKARYOTA: GRACILICUTES: SCOTOBACTERIA: FACULTATIVELY ANAEROBIC RODS;  
OC ENTEROBACTERIACEAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-T12;  
RX MEDLINE; 90008813.  
RA VERMA N., REEVES P.R.;  
RL J. BACTERIOL. 171:5694-5701(1989).  
[2]  
REVIEWS.  
RA REEVES P.R.;  
RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -1- CATALYTIC ACTIVITY: CDP-PARATOSE - CDP-TYPELOSE.  
CC -1- PATHWAY: FINAL STEP IN THE BIOSYNTHETIC PATHWAY OF CDP-TYPELOSE.  
CC -1- SIMILARITY: TO ABRDOSE AND PARATOSE SYNTHASES AND TO UDP-  
CC GLUCOSE-4-EPIMERASE OF E.COLI.  
DR EMBL; M29682; G861175; -.  
DR PIR; B33604; B33604.  
KW LIPOPOLYSACCHARIDE BIOSYNTHESIS; ISOMERASE.  
SQ SEQUENCE 338 AA; 37958 MW; 12C22DD0 CRC32;  
Query Match 77.4%; Score 48; DB 1; Length 338;  
Best Local Similarity 100.0%; Pred. No. 4.87e+01;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 41 NLHML 45  
QY 52 NLHML 56

RESULT 14  
ID P2X6\_RAT STANDARD; PRT; 379 AA.  
AC P51579;  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
DE P2X PURINOCEPTOR 6 (ATP RECEPTOR) (P2X6) (PURINERGIC RECEPTOR).  
GN P2X6.  
OS RATIUS NORVEGICUS (RAT).  
OC EUMAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA;  
OC EUTHERIA: RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-CERVICAL GANGLION;  
RX MEDLINE; 96256686  
RA COLLO G., KAMASHIMA E., PICH E., NEIDHART S., NORTH R.A.,  
RA SUPRENANT A., BUELL G.N.;  
RL J. NEUROSCI. 16:2495-2507(1996).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SPRACHE-DANLEY; TISSUE-BRAIN;  
RX MEDLINE; 96264662.  
RA SOTO F., GARCIA-GUZMAN M., KARSCHIN C., STUEHNER W.,  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 223:456-460(1996).  
CC -1- FUNCTION: RECEPTOR FOR ATP THAT ACTS AS A LIGAND GATED ION  
CC CHANNEL.  
CC -1- SUBUNIT: HOMO- OR HETEROPOLYMERS (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
DR EMBL; X92070; E205329; -.  
DR EMBL; X97376; E242827; -.  
DR PROSITE; PS01212; P2X\_RECEPTOR; 1.

KW IONIC CHANNEL; TRANSMEMBRANE; ION TRANSPORT; RECEPTOR; GLYCOPROTEIN.  
FT DOMAIN 1 31  
FT TRANSMEM 32 52  
FT DOMAIN 53 325  
FT TRANSMEM 326 346  
FT DOMAIN 347 379  
FT CARBOHYD 157 157  
FT CARBOHYD 187 187  
FT CARBOHYD 202 202  
SQ SEQUENCE 379 AA; 42450 MW; BB28CD0D CRC32;  
Query Match 77.4%; Score 48; DB 1; Length 379;  
Best Local Similarity 83.3%; Pred. No. 4.87e+01;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 257 GINLHW 262  
QY 50 GINLHW 55

RESULT 15  
ID TNAI\_ECOLI STANDARD; PRT; 471 AA.  
AC P00913; P78123;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
DE TRYPTOPHANASE (EC 4.1.99.1) (L-TRYPTOPHAN INDOLE-LYASE) (TNASE).  
GN TNAI OR IND.  
OS ESCHERICHIA COLI.  
OC PROKARYOTA: GRACILICUTES: SCOTOBACTERIA: FACULTATIVELY ANAEROBIC RODS;  
OC ENTEROBACTERIACEAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE; 82007678.  
RA DELEY M.C., YANOFSKY C.;  
RL J. BACTERIOL. 147:787-796(1981).  
[2]  
RP SEQUENCE FROM N.A., AND IMPORTANCE OF CYS-298.  
RC STRAIN-B/17-A;  
RX MEDLINE; 89323226.  
RA TOKUSHIGE M., TSUJIMOTO N., ODA T., HONDA T., YUMOTO N., ITO S.,  
RA YAMAMOTO M., KIM E.H., HIRAGI Y.;  
RL BIOCHIMIE 71:711-720(1989).  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE; 93315143.  
RA BURLAND V.D., PLUNKETT G. III, DANIELS D.L., BLATTNER F.R.;  
RL GENOMICS 16:551-561(1993).  
[4]  
RP SEQUENCE OF TRYPTIC PEPTIDES.  
RC STRAIN-K12;  
RX MEDLINE; 72134434.  
RA KAGAMIYAMA H., MATSUBARA H., SNELL E.E.;  
RL J. BIOL. CHEM. 247:1576-1586(1972).  
[5]  
RP SEQUENCE OF 1-21 FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE; 86033634.  
RA STEWART V., YANOFSKY C.;  
RL J. BACTERIOL. 164:731-740(1985).  
[6]  
RP SEQUENCE OF 463-471 FROM N.A.  
RX MEDLINE; 91216998.  
RA SARSERO J.P., WOOLLEY P.J., GOLINICK P.D., YANOFSKY C., PITTARD A.J.;  
RL J. BACTERIOL. 173:3231-3234(1991).  
[7]  
RP SEQUENCE OF 1-12.  
RC STRAIN-K12 / EMG2;  
RA LINK A.J.;  
RL SUBMITTED (OCT-1994) TO THE SWISS-PROT DATA BANK.  
[8]

RP MUTAGENESIS OF CYS-294 AND CYS-298. ---  
RX MEDLINE: 89278130.  
RA PHILLIPS R.S., GOLINICK P.D.;  
RL J. BIOL. CHEM. 264:10627-10632(1989).  
CC -1- CATALYTIC ACTIVITY: L-TRYPTOPHAN + H(2)O = INDOLE + PYRUVATE +  
CC NH(3) (ALSO CATALYZES THE SYNTHESIS OF TRYPTOPHAN FROM INDOLE  
CC AND SERINE).  
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -1- SUBUNIT: HOMOTETRAMER.  
CC -1- SIMILARITY: HIGH, TO TYROSINE PHENOL-LYASE.  
DR EMBL: K00032; G147997; -.  
DR EMBL: X15974; G41936; -.  
DR EMBL: M11990; G148001; -.  
DR EMBL: M59914; -; NOT ANNOTATED CDS.  
DR EMBL: L10328; G290556; ALT\_INIT.  
DR EMBL: AE000448; G1790144; ALT\_INIT.  
DR PIR: A01136; WZEC.  
DR HSSP: P31013; 1TPL.  
DR ECO2DBASE: G046.5; 6TH EDITION.  
DR ECOGENE: EG11005; TNA.  
DR PROSITE: PS00853; BETA\_ELIM\_LYASE.1.  
DR TRYPTOPHAN BIOSYNTHESIS; LYASE; PYRIDOXAL PHOSPHATE.  
KM TRYPTOPHAN BIOSYNTHESIS; LYASE; PYRIDOXAL PHOSPHATE.  
FT BINDING 270 270  
FT MUTAGEN 294 294 C->S: IDENTICAL TO WILD-TYPE.  
FT MUTAGEN 298 298 C->S: ALTERED ACTIVITY.  
FT CONFLICT 137 140 DTTO -> TTGG (IN REF.1).  
FT CONFLICT 379 380 OA -> TG (IN REF.1 AND 2).  
SQ SEQUENCE 471 AA: 32773 MW: 3724A677 CRC32;  
  
Query Match 77.4%; Score 48; DB 1; Length 471;  
Best Local Similarity 71.4%; Pred. No. 4,87e+01;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
DB 325 GMINLHWL 331  
QY 50 GINLHWL 56

Search completed: Tue Apr 20 14:05:02 1999  
Job time : 7 secs.

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Apr 20 14:05:20 1999; MasPar time 4.35 Seconds
Tabular output not generated. 80.112 Million cell updates/sec

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Title: >US-08-836-455-1_1
Description: (50-56) from trans.pep (2 of 3)
Perfect Score: 62
Sequence: 1 GINLHWL 7

```

Scoring table: PAM 150  
Gap 11

```
Searched:      165420 seqs, 49795644 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
```

1:sp\_archaea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human  
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle  
9:sp\_plage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified  
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 23.380; Variance 35.189; scale 0.664

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	58	93.5	964	2	053784	PUTATIVE MEMBRANE PROT	1.45E+00
2	53	85.5	967	2	053735	PUTATIVE TRANSMEMBRANE	1.15E+00
3	50	80.6	188	2	P71161	INTB, REGA, GEPA, GEPB	3.74E+00
4	50	80.6	372	2	P95323	HYPOTHELICAL 41.3 KD P	3.74E+00
5	50	80.6	386	11	Q60962	CARCINOEMBRYONIC ANTIG	3.74E+00
6	50	80.6	435	5	Q21859	R09D1.3	3.74E+00
7	50	80.6	476	2	Q67845	GLUTAMATE SYNTHASE SMA	3.74E+00
8	50	80.6	667	2	Q05069	TRANSPPOSASE A (MDA)	3.74E+00
9	50	80.6	707	2	Q50198	TONB-DEPENDENT RECEPTO	3.74E+00
10	50	80.6	791	2	Q25543	IRON-REGULATED OUTER M	3.74E+00
11	50	80.6	1135	11	Q64700	RETINOBLASTOMA-LIKE 2	3.74E+00
12	50	80.6	1135	11	Q05681	P130.	3.74E+00
13	50	80.6	1139	4	Q16084	P130.	3.74E+00
14	50	80.6	1139	4	Q15073	HEPOTIC PROTEIN.	3.74E+00
15	49	79.0	322	2	Q51122	HEPOTIC TRANSFERASE I.	5.49E+00
16	49	79.0	332	2	Q50937	LIPOLIGOSACCHARIDE HE	5.49E+00
17	49	79.0	336	2	Q51128	1.5 HEPOTIC TRANSFERAS	5.49E+00
18	49	79.0	332	2	Q50177	SUCCINYLGLUTAMATE DESU	5.49E+00
19	49	79.0	351	2	P73167	HYPOTHELICAL 42.6 KD P	5.49E+00
20	49	79.0	521	5	Q21360	K06B8.1.	5.49E+00

21	49	79.0	577	5	023616	ZR622.5	5.49e+01
22	49	79.0	811	5	093382	HYDROLYTICAL PROTEIN C	5.49e+01
23	49	79.0	996	6	P71448	BETA-D-GALACTOSIDASE.	5.49e+01
24	49	79.0	998	2	Q48727	BETA-GALACTOSIDASE.	5.49e+01
25	48	77.4	129	5	F49C5.5	F49C5.5.	8.03e+01
26	48	77.4	205	1	059366	S25AA LONG HYPONHETICA	8.03e+01
27	48	77.4	227	14	066496	NR9A1 LONG ORF2.	8.03e+01
28	48	77.4	248	5	062113	C47F8.4.	8.03e+01
29	48	77.4	264	2	059537	LIPASE-ESTERASE (EC 3.	8.03e+01
30	48	77.4	328	5	017940	K08F9.3.	8.03e+01
31	48	77.4	338	3	000047	ISOPENICILLIN N SYNTHET	8.03e+01
32	48	77.4	347	11	035789	GLYCOPROTEIN SPECIFIC	8.03e+01
33	48	77.4	458	5	022675	T22C8.2.	8.03e+01
34	48	77.4	562	12	052551	V5A.	8.03e+01
35	48	77.4	562	14	082511	HEMAGGLUTININ PRECURSO	8.03e+01
36	48	77.4	622	11	093736	TRANSFERIN RECEPTOR P	8.03e+01
37	48	77.4	637	3	092199	PUTATIVE TRANSPOSASE.	8.03e+01
38	48	77.4	757	11	007891	TRANSFERIN RECEPTOR P	8.03e+01
39	48	77.4	763	11	062351	TRANSFERIN RECEPTOR.	8.03e+01
40	48	77.4	810	4	012830	FETAL ALF-50-REACTIVE	8.03e+01
41	48	77.4	821	5	018423	HYPONHETICAL PROTEIN C	8.03e+01
42	48	77.4	858	5	024335	REVERSE TRANSCRIPTASE	8.03e+01
43	48	77.4	888	5	004135	PUTATIVE RNA-DIRECTED	8.03e+01
44	47	75.8	346	5	061659	SELECTIN I (FRAGMENT).	1.17e+02
45	47	75.8	932	13	073626	ACID ALPHA GLUCOSIDASE	1.17e+02

## ALIGNMENTS

RESULT	1	PRELIMINARY;	PRF;	964	AA.
ID	053784				
AC	053784;				
DT	01-JUN-1998	(TREMBLREL. 06,	CREATED)		
DT	01-JUN-1998	(TREMBLREL. 06,	LAST SEQUENCE UPDATE)		
DT	01-JUN-1998	(TREMBLREL. 06,	LAST ANNOTATION UPDATE)		
DE	PUTATIVE MEMBRANE PROTEIN.				
GN	MTV040.04c.				
OS	MYCOBACTERIUM TUBERCULOSIS.				
OC	PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-H37RV;				
RA	HAMILIN N., CHURCHER C.M.;				
RL	SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-H37RV;				
RA	COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;				
RL	SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-H37RV;				
RA	MEDLINE; 96181548.				
RL	PHILIPP W.J., POULET S., EIGMEIER K., PASCOPELLA L.,				
RA	BALASUBRAMANIAN V., HEYM B., BERKH S., BLOOM B.R., JACOBS W.R. JR.,				
RL	COLE S.T.;				
RA	PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).				
DR	EMBL; AL021943; E1253102; "				
SO	SEQUENCE	964	AA;	104784	MM; BA29E3A3 CRC32;
Query Match					
Best Local Similarity		85.7%;	Score 58;	DB 2;	Length 964;
Matches		6;	Conservative	1;	Mismatches 0;
Indels		0;	Gaps	0	
Db	828 GINLHMT	834			
QY	50 GINLHMT	56			
RESULT 2					
ID	053735	PRELIMINARY;	PRT;	967	AA.
AC	053735;				
DT	01-JUN-1998	(TREMBLREL. 06,	CREATED)		

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE PUTATIVE TRANSMEMBRANE PROTEIN.  
 GN MT0037.14C.  
 OS MYCOBACTERIUM TUBERCULOSIS.  
 OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RA BROWN D., CHURCHER C.M.;  
 RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RA COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;  
 RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RA PHILIPPE W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,  
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,  
 RA COLE S.T.;  
 RA PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).  
 DR EMBL; AL021932; E1252519;  
 KW TRANSMEMBRANE.  
 SQ SEQUENCE 967 AA; 105233 MW; 3957DF42 CRC32;

Query Match 85.5%; Score 53; DB 2; Length 967;  
 Best Local Similarity 71.4%; Pred. No. 1.15e+01;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 823 A1HLHML 829  
 QY 50 G1NLHML 56  
 ID 1:111111

RESULT 3  
 ID P71161 PRELIMINARY; PRT; 198 AA.  
 AC P71161;  
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)  
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DE INTB, REGA, GEPA, GEPA, AND GEPC GENES.  
 GN INTB, REGA, GEPA, GEPA, AND GEPC GENES.  
 OS BACTERIOIDES NODOSUS (DICHELIOBACTER NODOSUS).  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; ANAEROBIC RODS;  
 BACTEROIDACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A198;  
 RA BLOOMFIELD G.A., WHITTLE G., McDONNIGH M.B., KATZ M.E., CHEETHAM B.F.;  
 RL MICROBIOLOGY 143:553-562(1997).  
 DR EMBL; X98546; E258655;  
 SQ SEQUENCE 198 AA; 21550 MW; FA6F6C9D CRC32;

Query Match 80.6%; Score 50; DB 2; Length 198;

Best Local Similarity 83.3%; Pred. No. 3.74e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 157 I1LHML 162  
 QY 51 I1LHML 56  
 ID 1:111111

RESULT 4  
 ID P95233 PRELIMINARY; PRT; 372 AA.  
 AC P95233;  
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)  
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)  
 DT 01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)  
 DE HYPOTHEICAL 41.3 KD PROTEIN.  
 GN M1CY98.06C.

OS MYCOBACTERIUM TUBERCULOSIS.  
 OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA BROWN D., CHURCHER C.M.;  
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA COLE S.T., BARRELL B.G., RAJANDREAM M.A.;  
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE; 96181548.  
 RA PHILIPPE W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,  
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,  
 RA COLE S.T.;  
 RA PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).  
 DR EMBL; Z83860; E290744;  
 KW HYPOTHEICAL PROTEIN.  
 SQ SEQUENCE 372 AA; 41272 MW; A4F94BDE CRC32;

Query Match 80.6%; Score 50; DB 2; Length 372;  
 Best Local Similarity 71.4%; Pred. No. 3.74e+01;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 154 G1OLHMF 160  
 QY 50 G1NLHML 56  
 ID 1:111111

RESULT 5  
 ID O60962 PRELIMINARY; PRT; 386 AA.  
 AC O60962;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE CARCINOEMBRYONIC ANTIGEN 11 (BRAIN CARCINOEMBRYONIC ANTIGEN).  
 GN CE11 OR BCEA.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA MEDLINE; 96109212.  
 RA CHEN D.S., ASANAKA M., YOKOMORI K., WANG F., HWANG S.B., LI H.P.,  
 RA LAI M.M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 92:12095-12099(1995).  
 DR EMBL; U34272; G1098896;  
 DR MGD; MGI:104983; CE11.  
 DR PFAM; PF00047; 15;  
 SQ SEQUENCE 386 AA; 43362 MW; E1EA398E CRC32;

Query Match 80.6%; Score 50; DB 1; Length 386;

Best Local Similarity 57.1%; Pred. No. 3.74e+01;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 323 GVS1HML 329  
 QY 50 G1NLHML 56  
 ID 1:1:111111

RESULT 6  
 ID O21859 PRELIMINARY; PRT; 435 AA.  
 AC O21859;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DE R09D1.3.  
 OS CAENORHABDITIS ELEGANS.  
 OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA MATTHEWS P.;  
 RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA BURSON J., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,  
 RA DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P.,  
 RA HAWKINS T., HILLER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,  
 RA KIRSTEN J., LAISTER N., LATREILLE P., LIGHTING J., LLOYD C.,  
 RA MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,  
 RA RIEPEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SHALON N., SMITH A.,  
 RA SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K.,  
 RA VAUDIN M., VAGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,  
 RA WILKINSON-SPROAT J., WOHLDMAN P.;  
 RL NATURE 368:32-38(1994).  
 DR EMBL: 270035: E228187;  
 DR PFAM: PF00704; glycosyl\_hydrol.  
 SQ SEQUENCE 435 AA; 50487 MW; C05D5854 CRC32;  
 Query Match 80.6%; Score 50; DB 5; Length 435;  
 Best Local Similarity 66.7%; Pred. No. 3,74e+01;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 DB 182 GVDLHW 187  
 QY 50 GINLHW 55  
 RESULT 7  
 ID 067845; PRELIMINARY; PRT: 476 AA.  
 AC 067845;  
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DE GLUTAMATE SYNTHASE SMALL SUBUNIT GLTD.  
 GN GLTD.  
 OS AQUIFEX AEOLICUS.  
 OC EUBACTERIA; AQUIFACLES; AQUIFACACEAE; AQUIFEX.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-VF5;  
 RA DECKERT G., WARREN P.V., GASTERLAND T., YOUNG W.G., LENOX A.L.,  
 RA GRAHAM D.E., OVERBEER R., SNEAD M.A., KELLER M., ANJAY M., HUBER R.,  
 RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;  
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: AE000770; G2984275;  
 SQ SEQUENCE 476 AA; 52947 MW; 97B08285 CRC32;  
 Query Match 80.6%; Score 50; DB 2; Length 476;  
 Best Local Similarity 57.1%; Pred. No. 3,74e+01;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 DB 342 GVKIHWL 348  
 QY 50 GINLHWL 56  
 RESULT 8  
 ID 005069; PRELIMINARY; PRT: 687 AA.  
 AC 005069;  
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)  
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)  
 DT 01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)  
 DE TRANSPOSASE A (MOA).  
 GN HI1478.  
 OS HAEMOPHILUS INFLUENZAE.

OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC PASTURELLACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 95350630.  
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,  
 RA KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.,  
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,  
 RA SCOTT J.D., SHIRLEY R., LIU L.I., GLODER A., KELLEY J.M., WEIDMAN J.F.,  
 RA PHILLIPS C.A., SPRIGGS T., HEDBLOW E., COTTON M.D., UTERBACK T.R.,  
 RA HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., PINE L.D.,  
 RA FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GHEH C.L.,  
 RA MCDONALD L.A., SWALL K.V., FRASER C.M., SMITH H.O., VENTER J.C.;  
 RL SCIENCE 269:496-512(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA I TATUSOV R., MOSHEGIAN A.R., BORK P., BROWN N.P., HAYES W.S.,  
 RA BORODOVSKY M., RUDD K.E., KOONIN E.V.;  
 RL CURR. BIOL. 6:279-291(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,  
 RA KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.,  
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,  
 RA SCOTT J.D., SHIRLEY R., LIU L.I., GLODER A., KELLEY J.M., WEIDMAN J.F.,  
 RA PHILLIPS C.A., SPRIGGS T., HEDBLOW E., COTTON M.D., UTERBACK T.R.,  
 RA HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., PINE L.D.,  
 RA FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GHEH C.L.,  
 RA MCDONALD L.A., SWALL K.V., FRASER C.M., SMITH H.O., VENTER J.C.;  
 RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;  
 RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: U32825; G1574318;  
 SQ SEQUENCE 687 AA; 78719 MW; A4C0045E CRC32;  
 Query Match 80.6%; Score 50; DB 2; Length 687;  
 Best Local Similarity 83.3%; Pred. No. 3,74e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 DB 379 GIELHW 384  
 QY 50 GINLHW 55

RESULT 9  
 ID 050198; PRELIMINARY; PRT: 707 AA.  
 AC 050198;  
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE TONB-DEPENDENT RECEPTOR HOMOLOG (FRAGMENT).  
 OS HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;  
 OC AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-RU1;  
 RA MANOS J., KOLESNIKOV T., HAZELL S.L.;  
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: AF015886; G265532;  
 FT NON-TER 707  
 SQ SEQUENCE 707 AA; 79095 MW; B82B1B54 CRC32;  
 Query Match 80.6%; Score 50; DB 2; Length 707;  
 Best Local Similarity 85.7%; Pred. No. 3,74e+01;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 DB 665 GINLHWL 671  
 QY 50 GINLHWL 56



SO SEQUENCE 1139 AA; 128365 MW; 2F0C942B CRC32;

Query Match 80.6%; Score 50; DB 4; Length 1139;

Best Local Similarity 71.4%; Pred. NO. 3.74e+01;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 81 GNDLHNL 87  
1 :|||||  
50 GINLHNL 56

RESULT 14  
ID 015073 PRELIMINARY; PRT; 1139 AA.

AC 015073;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DE 130K PROTEIN.

GN P130.

HO HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE-PLACENTA/SPLEEN;

RX MEDLINE: 94074895.

RA LI Y., GRAHAM C., LACY S., DUNCAN A.M.V., WHITE P.;

RL GENES DEV. 7:2366-2377(1993).

DR EMBL: X76061; G416031; -

SO SEQUENCE 1139 AA; 128381 MW; 659C515E CRC32;

Query Match 80.6%; Score 50; DB 4; Length 1139;  
Best Local Similarity 71.4%; Pred. NO. 3.74e+01;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 81 GNDLHNL 87  
1 :|||||  
50 GINLHNL 56

RESULT 15  
ID 051122 PRELIMINARY; PRT; 322 AA.

AC 051122;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)

DE HEPATOSYLTRANSFERASE I.

RFAC.

NEISSERIA MENINGITIDIS.

OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;

OC NEISSERIACEAE.

RN (1)

RP SEQUENCE FROM N.A.

RA ZHOU D., LEE F.F., APICELIA M.A.;

RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: U35454; G1016752; -

KW TRANSFERASE.

SO SEQUENCE 322 AA; 36188 MW; 8276FA9F CRC32;

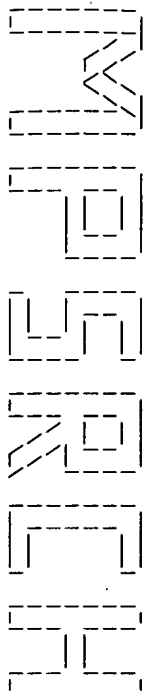
Query Match 79.0%; Score 49; DB 2; Length 322;  
Best Local Similarity 66.7%; Pred. NO. 5.49e+01;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 31 VELHNL 36  
1 :|||||  
51 INLHNL 56

Search completed: Tue Apr 20 14:05:51 1999  
Job time : 31 secs.

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(TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
on: Tue Apr 20 14:08:59 1999; Maspar time 2.57 Seconds  
56.748 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-836-455-1\_1  
Description: (89-97) from trans. pep (3 of 3)  
Perfect Score: 54  
Sequence: 1 SDYSLRTSS 9

Scoring table: PAM 150  
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

a-geneseq32  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29

Statistics: Mean 15.830; Variance 48.580; scale 0.336

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	54	100.0	95	25	W18269	Prp 81 light chain va	1.90e+01
2	54	100.0	107	29	W44122	Light chain variable	1.90e+01
3	54	100.0	107	25	W27121	Murine antibody light	1.90e+01
4	54	100.0	108	4	R21310	Light chain of Mlf c1	1.90e+01
5	54	100.0	108	4	R21286	Murine V $\lambda$ kappa group	1.90e+01
6	54	100.0	109	25	W18271	Prp 37 light chain va	1.90e+01
7	54	100.0	109	18	R52030	Light chain variable	1.90e+01
8	54	100.0	129	24	W22537	Murine anti-human cla	1.90e+01
9	54	100.0	145	25	W27119	Murine monoclonal ant	1.90e+01
10	54	100.0	146	4	P30251	Sequence of the laede	1.90e+01
11	54	100.0	243	18	W02280	520C9 anti-c-erbB-2 t	1.90e+01
12	54	100.0	246	8	R39569	Sequence of 520C9 sfv	1.90e+01
13	54	100.0	534	8	R39571	Sequence of G-FIT	1.90e+01
14	52	96.3	107	29	W44123	Light chain variable	3.15e+01
15	52	96.3	127	6	R32125	Anti-IL2R alpha antib	3.15e+01
16	52	96.3	144	3	R15322	IL-2 chimeric antibod	3.15e+01
17	52	96.3	144	3	R15321	IL-2 chimeric antibod	3.15e+01
18	51	94.4	107	14	R79247	Light chain variable	4.05e+01

19	51	94.4	107	14	R78972	Light chain variable	4.05e+01
20	51	94.4	107	14	R79250	Light chain variable	4.05e+01
21	50	92.6	106	28	W1647	Monoclonal antibody C	5.19e+01
22	50	92.6	107	29	W23956	Mus musculus A717 ant	5.19e+01
23	50	92.6	107	25	W24515	Anti-Factor-IX human	5.19e+01
24	50	92.6	109	25	W24530	Anti-Factor-IX human	5.19e+01
25	50	92.6	109	26	W29997	Humanised variant of	5.19e+01
26	50	92.6	109	26	W29995	Light chain variable	5.19e+01
27	50	92.6	125	25	W24517	Anti-Factor-IX human	5.19e+01
28	50	92.6	128	10	R53332	KM-603 light chain	5.19e+01
29	50	92.6	129	25	W24518	Anti-Factor-IX human	5.19e+01
30	50	92.6	214	26	W34506	Light chain of full 1	5.19e+01
31	50	92.6	214	26	W34504	Light chain of human	5.19e+01
32	50	92.6	214	24	W27089	Mouse monoclonal anti	5.19e+01
33	50	92.6	228	26	R14704	V1-lab-Vh constructio	5.19e+01
34	50	92.6	233	6	R30777	PH52-9.0 humanised mu	5.19e+01
35	50	92.6	233	3	R14695	V1-lab-Vh constructio	5.19e+01
36	50	92.6	250	25	W29261	Anti-c-erbB-2 single	5.19e+01
37	50	92.6	250	23	W22400	Single chain antibody	5.19e+01
38	50	92.6	264	27	W35562	HindIII-EcoRI insert	5.19e+01
39	50	92.6	355	28	W35125	R. pipiens recombinan	5.19e+01
40	50	92.6	355	28	W35129	R. pipiens recombinan	5.19e+01
41	50	92.6	358	28	W35127	R. pipiens recombinan	5.19e+01
42	50	92.6	358	28	W35130	R. pipiens recombinan	5.19e+01
43	50	92.6	360	28	W35128	R. pipiens recombinan	5.19e+01
44	50	92.6	379	28	W35126	R. pipiens recombinan	5.19e+01
45	50	92.6	532	27	W35565	HindIII-EcoRI insert	5.19e+01

## ALIGNMENTS

RESULT 1	W18269 standard; peptide: 95 AA.
AC	W18269;
DR	09-JAN-1998 (first entry)
DE	Prp 81 light chain variable region.
KW	Prion protein; Prp; heavy chain variable region; antibody; scrapie;
KW	light chain variable region; Prp-Sc; pathogen; fatal familial insomnia;
KW	central nervous system spongiform encephalopathy; human; therapy;
KW	transmissible neurodegenerative disease; Creutzfeldt-Jakob disease;
KW	bovine spongiform encephalopathy; feline spongiform encephalopathy;
KW	Serretmann-Stressler-Scheinker Disease.
OS	Mus musculus.
FH	Key
FT	Region
FT	Location/Qualifiers
FT	1..9
FT	/note= "framework region 1"
FT	Misc_difference 3
FT	/note= "unspecified amino acid"
FT	Region
FT	10..20
FT	/note= "complementarity determining region 1"
FT	Region
FT	21..35
FT	/note= "framework region 2"
FT	Region
FT	36..42
FT	/note= "complementarity determining region 2"
FT	Region
FT	43..74
FT	/note= "framework region 3"
FT	Region
FT	75..88
FT	/note= "complementarity determining region 3"
FT	Region
FT	89..95
FT	/note= "framework region 4"
PN	W09710505-A1.
PD	20-MAR-1997.
PF	13-SEP-1996; U14840.
PR	14-SEP-1995; US-528104.
PA	(RECC) UNIV CALIFORNIA.
PI	Burton DR, Prusiner SB, Williamson RA;
DR	WPI: 97-202357/18.
PT	New antibodies to the scrapie isoform of prion protein - used for
PT	detection of infectious prion proteins or for treating disease such
PT	as BSE, CJD or scrapie
PT	Example 9; Fig 6; 99pp; English.
CC	W18266-W18285 represent portions of the antibodies of the invention. The
CC	antibodies of the invention are able to bind the scrapie isoform of prion

CC protein PrP-Sc in situ. Prions are infectious pathogens that cause  
 CC central nervous system spongiform encephalopathies in humans and animals.  
 CC The scrapie isoform of the prion protein (PrP-Sc) is necessary for both  
 CC the transmission and pathogenesis of the transmissible neurodegenerative  
 CC diseases of animals and humans. The antibodies can be used in a method of  
 CC the invention for detecting human PrP-Sc in a source. The antibodies  
 CC specifically bind to prion proteins associated with disease and do not  
 CC bind to denatured PrP proteins not associated with disease. They can also have  
 CC the ability to neutralise infectious prions. The antibodies can be used  
 CC for screening for the presence of prions in products such as  
 CC pharmaceuticals, food or cosmetics. They can also be used for prion  
 CC neutralisation to purify products, for extraction of prion proteins or  
 CC for therapy, for diseases such as bovine spongiform encephalopathy,  
 CC Creutzfeldt-Jakob Disease, fatal familial insomnia or  
 CC Serzmann-Strassler-Scheinker Disease, scrapie or feline spongiform  
 CC encephalopathies.  
 SQ Sequence 95 AA;

Query Match 100.0%; Score 54; DB 25; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 1.90e+01;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 sdsylists 63  
 OY 89 SDYSLISTS 97

RESULT 2  
 ID W4122 standard; Protein; 107 AA.  
 AC W4122;

DE 05-JUN-1998 (first entry)  
 DE Light chain variable region of NR-LU-13 antibody.

KW Light chain; variable region; murine; mouse; human; cancer antigen;  
 KW antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;

OS Mus sp.

FT Key Location/Qualifiers

FT Region 24..34 /note- "complementarity determining region 1"

FT Region 50..56 /note- "complementarity determining region 2"

FT Region 89..97 /note- "complementarity determining region 3"

PN MO9746589-A2.

PD 11-DEC-1997.

06-JUN-1997; 010074.

07-JUN-1996; US-660362.

(NEOR-) NEORX CORP.  
 PI Graves SS, Henry AH, Hyalarides MD, Mallet RW, Pedersen JT,

PI Rees AR, Rencio JM, Searle SMJ;  
 DR WPI: 98-042124/04.

DR N-PSDB; V02198.

PT Humanised antibody binds same human cancer antigen as antibody

PT NR-LU-13 - useful for pre-targeting methods, conventional antibody

PS Example 1: Fig 2: 100pp: English.

CC The present sequence is the light chain variable region of the

CC murine anti-human cancer antigen antibody (Ab) NR-LU-13.

CC A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. The

CC hAb, specifically NRX451, or its conjugates can be used for the

CC manufacture of a diagnostic or medicament for cancer diagnosis or

CC treatment. The hAb has reduced immunogenicity and toxicity in

CC humans, but retains the ability to bind the NR-LU-13 antigen.

SQ Sequence 107 AA;

Query Match 100.0%; Score 54; DB 29; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 1.90e+01;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 69 sdsylists 77  
 OY 89 SDYSLISTS 97

RESULT 3  
 ID W27121 standard; Protein; 107 AA.  
 AC W27121;

DE 04-JAN-1998 (first entry)

DE Murine antibody light chain variable region consensus.

KW Monoclonal antibody 11D10; anti-Idiotypic antibody; mAb;  
 KW human milk fat globule; HMG; tumour; breast cancer; vaccine.

OS Mus musculus.

FT Key Location/Qualifiers

FT Region 24..34 /label- CDR1

FT Region 50..56 /note- "complementarity determining region 1"

FT Region 88..96 /label- CDR2

FT Region 88..96 /label- CDR3

FT Region 88..96 /note- "complementarity determining region 2"

FT Region 88..96 /note- "complementarity determining region 3"

PN MO9722699-A2.

PD 26-JUN-1997.

PE 19-DEC-1996; U20757.

PR 13-DEC-1996; US-575762.

PR 20-DEC-1995; US-575762.

PR 26-JAN-1996; US-591965.

PA (KENT) UNIV KENTUCKY.

PI Chatterjee M, Chatterjee SK, Foon KA;

DR WPI: 97-341690/31.

PT Monoclonal anti-Idiotypic antibody 11D10 - elicits immune response

PT against human milk fat globule disease associated tumours,

PT especially breast cancer

PS Example 2: Fig 26C; 130pp; English.

CC This polypeptide sequence comprises a consensus sequence of murine

CC light chain variable regions (VR) selected on the basis of identity

CC to the VR region (see W27121) of monoclonal anti-Idiotypic antibody

CC 11D10. The sequences were obtained from a GenBank database

CC search. A VR consensus (W27122) was also produced. 11D10 has at

CC least 18 departures from the consensus sequences (7 in the light

CC chain and 11 in the heavy chain). 8 occur within CDRs and 10

CC outside CDRs. 11D10 polypeptides and polynucleotides can be

CC used in vaccines and pharmaceutical compositions for the treatment

CC of human milk fat globule-associated diseases such as breast

CC cancer.

SQ Sequence 107 AA;

Query Match 100.0%; Score 54; DB 25; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 1.90e+01;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 69 sdsylists 77  
 OY 89 SDYSLISTS 97

RESULT 4  
 ID R21310 standard; Protein; 108 AA.  
 AC R21310;

DE 21-MAY-1992 (first entry)

DE Light chain of Mf clone

KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;

KW plus; g3p; binding; adsorption; gene VIII; diverse repertoire;

OS Specific binding pairs; replicable genetic display package.

FT Key Location/Qualifiers

FT Region 25..34 /label- CDR1

FT Region 50..56 /label- CDR2

FT Region 89..96 /label- CDR3

PN MO9201047-A.

PD 23-JAN-1992.

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PF 10-JUL-1991; G01134.
PR 10-JUL-1990; GB-015198.
PR 19-OCT-1990; GB-022845.
PR 12-NOV-1990; GB-024503.
PR 06-MAR-1991; GB-004744.
PR 15-MAY-1991; GB-010549.
PA (CMB-) CAMBRIDGE ANTIBODY.
PA (MED-) MED RES COUNCIL.
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Jackson TP, Chiswell DJ;
PI Winter GP, Bonnett TP;
DR WPI; 92-056862/07.
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
PS Example 46; Fig 52; 109pp; English.
CC The sequence is the light chain of clone M1F encoding an scFv frag-
CC ment specific for both hen and turkey egg lysozyme (HEL and TEL).
CC The DNA encoding the chain was amplified from a cDNA library prepd.
CC from the spleen of an unimmunised mouse. The corresponding heavy
CC chain was also amplified from an existing construct, pSW1-VHD1.3
CC (Ward et al, 1989). The two fragments were assembled via a linker
CC to prepare an scFv construct which was ligated into the fdCAT2
CC vector for expression on the surface of fd bacteriophage. In this
CC way, the VL domain was replaced by a library of VL domains to allow
CC for selection of a broader range of antibody specificities. Several
CC clones were isolated which bound to TEL (the parent antibody D1.3
CC binds exclusively to HEL). The sequences of the light chains of
CC two of these clones, MFI and M21 are given in R21310 and R21311
CC respectively. The D1.3 light chain is given in R21309.
CC See also R21260-307, 309-312, R22450, R22565, R22567-81.
CC Sequence 108 AA;
SQ
Query Match 100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.90e+01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 69 sdsylists 77
QY 89 SDYSLISTS 97
RESULT 5
ID R21286 standard; Protein: 108 AA.
AC R21286;
DE 21-MAY-1992 (first entry)
DE Murine VL kappa group V chain "a", specific for phox.
DE fd; bacteriophage; gene III; filamentous; phageid; coat;
DE plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package.
OS Synthetic.
FH Key Location/Qualifiers
FT binding-site 24..34
FT binding-site /label= CDR1
FT binding-site 50..56
FT binding-site /label= CDR2
FT binding-site 89..96
FT binding-site /label= CDR3
FT /note="D-X-G-X-X motif"
PN MO9201047-A.
PD 23-JAN-1992.
PF 10-JUL-1991; G01134.
PR 10-JUL-1990; GB-015198.
PR 19-OCT-1990; GB-022845.
PR 12-NOV-1990; GB-024503.
PR 06-MAR-1991; GB-004744.
PR 15-MAY-1991; GB-010549.
PA (CMB-) CAMBRIDGE ANTIBODY.
PA (MED-) MED RES COUNCIL.
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Jackson TP, Chiswell DJ;
PI Winter GP, Bonnett TP;
DR WPI; 92-056862/07.

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PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
PS Example 21; Fig 24; 209pp; English.
CC The VR sequence is one of seven (R21286-92) found to be expressed
CC from a single chain Fv library from an immunised mouse. The libra-
CC ry produces a diverse repertoire of antibody fragments specific for
CC 2-phenyl-5-oxazolone (phox). It was prepd. using cDNA generated
CC from mRNA from mice immunised with phox coupled to chicked serum
CC albumin. The VH and VL kappa sequences were separately amplified
CC by PCR (see Q23474-84) and ligated into fdCAT2 (see Q23463) for ex-
CC pression on the phage surface as fusions with gene III. The result-
CC ing library of clones was diverse. Twenty three hapten binding
CC clones were sequenced revealing eight different VH genes (A-H) (see
CC R21264-71) in a variety of pairings with the seven different VL
CC genes (a-g). Of the twenty three clones sequenced, three were of
CC type "a", and were "ox-like" genes. (See Berck et al, Nature 316
CC 413-418, 1985). They contain the DXGX motif in CDR3, the central
CC gly of which is needed to create a cavity for phox. Most of the
CC clones were Vκ-d combinations. The kd of Vκ-B/Vκ-d for phox-GABA
CC was 10 nM. Only two other combinations (of eleven tested) were
CC found to have higher values. This suggests that phage bearing scFv
CC fragments having weak affinities can be selected with antigen, pro-
CC bably due to the avidity of the multiple antibody heads on the
CC phage.
CC See also R21260-307, 309-311; R22450, 565-581.
CC Sequence 108 AA;
SQ
Query Match 100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.90e+01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 69 sdsylists 77
QY 89 SDYSLISTS 97
RESULT 6
ID W18271 standard; peptide: 109 AA.
AC W18271;
DE 09-JAN-1998 (first entry)
DE PRP 37 light chain variable region.
DE Prion protein; Prp; heavy chain variable region; antibody; scrapie;
KW light chain variable region; Prp-Sc; pathogen; fatal familial insomnia;
KW central nervous system spongiform encephalopathy; human; therapy;
KW transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease;
KW bovine spongiform encephalopathy; feline spongiform encephalopathy;
KW Serstmann-Stressler-Scheinker Disease.
OS Mus musculus.
FH Key Location/Qualifiers
FT Region 1.23
FT Region /note="framework region 1"
FT Region 24..34
FT Region /note="complementarity determining region 1"
FT Region 35..49
FT Region /note="framework region 2"
FT Region 50..56
FT Region /note="complementarity determining region 2"
FT Region 57..88
FT Region /note="framework region 3"
FT Region 89..97
FT Region /note="complementarity determining region 3"
FT Region 98..109
FT Region /note="framework region 4"
PN MO9710505-A1.
PD 20-MAR-1997.
PF 13-SEP-1996; U14840.
PR 14-SEP-1995; US-528104.
PA (REGC ) UNIV CALIFORNIA.
PI Burton DR, Prusiner SB, Williamson RA;
PI WPI; 97-202357/18.
PT New antibodies to the scrapie isoform of prion protein - used for
PT detection of infectious prion proteins or for treating disease such

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PT as BSE, CJD or scrapie  
 PS Example 9: Fig 6; 99pp; English.  
 CC W18266-W18285 represent portions of the antibodies of the invention. The  
 CC antibodies of the invention are able to bind the scrapie isoform of prion  
 CC protein PrP-Sc in situ. Prions are infectious pathogens that cause  
 CC the scrapie isoform of the prion protein (PrP-Sc) is necessary for both  
 CC the transmission and pathogenesis of the transmissible neurodegenerative  
 CC diseases of animals and humans. The antibodies can be used in a method of  
 CC the invention for detecting human PrP-Sc in a source. The antibodies  
 CC specifically bind to prion proteins associated with disease and do not  
 CC bind to denatured PrP proteins not associated with disease. They can bind  
 CC to prion proteins of a specific species of mammals. They can also have  
 CC the ability to neutralise infectious prions. The antibodies can be used  
 CC for screening for the presence of prions in products such as  
 CC pharmaceuticals, food or cosmetics. They can also be used for prion  
 CC neutralisation to purify products, for extraction of prion proteins or  
 CC for therapy, for diseases such as bovine spongiform encephalopathy,  
 CC Creutzfeldt-Jakob Disease, fatal familial insomnia or  
 CC Seemann-Strassler-Scheinker Disease, scrapie or feline spongiform  
 CC encephalopathies.  
 SO Sequence 109 AA:

Query Match 100.0%; Score 54; DB 25; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 1.90e+01;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 69 sdsyltiss 77  
 |||||  
 QY 89 SDYSLTSS 97

RESULT 7  
 ID R52030 standard; Protein; 109 AA.  
 AC R52030.

DT 26-SEP-1996 (first entry)  
 DE Light chain variable region of murine antibody g1b2.

KW antibody; humanised; murine; human; heavy chain; light; variable;  
 KM framework region; complementarity determining region; reshaping;  
 OS Mus sp.

PS Key  
 FT region 1..23 Location/Qualifiers  
 FT /label=framework\_region\_1  
 FT /note="FR 1"

FT region 24..34  
 /label=complementarity\_determining\_region\_1  
 /note="CDR 1"

FT region 35..49  
 /label=FR\_2  
 /note="CDR 2"

FT region 50..56  
 /label=CDR\_2  
 /note="CDR 2"

FT region 57..88  
 /label=FR\_3  
 /note="CDR 3"

FT region 89..97  
 /label=CDR\_3  
 /note="CDR 3"

FT region 98..109  
 /label=FR\_4  
 /note="FR 4"

PN EP-592106-A1.  
 PD 13-APR-1994.  
 PF 07-SEP-1993; 307051.  
 PR 09-SEP-1992; US-942245.

PA (PEDE-) PEDERSEN J T.  
 PI (IMMU-) IMMUNOGEN INC.  
 PT Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;  
 DR WPI: 94-120230/15.  
 PT Method of resurfacing of rodent antibodies to produce humanised  
 PT antibody forms - for producing non-human antibodies with improved  
 PT therapeutic efficiency by presenting human surface on V-region  
 PS Example 1; Fig 3A; 230pp; English.

CC The present sequence is that of the light chain variable (LC VR) region  
 CC of murine antibody g1b2. This sequence was aligned with 11 other known  
 CC antibody LC VRs and a set of framework positions of surface exposed amino

CC acid residues was determined. This information can be used in a method to  
 CC determine how to modify a rodent antibody or fragment by resurfacing in  
 CC order to produce a humanised rodent antibody. Residues (determined from  
 CC alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 53, 66, 73, 86,  
 CC 87, 111, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127,  
 CC 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142,  
 CC 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157,  
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 CC 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384,  
 CC 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397,  
 CC 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410,  
 CC 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422,  
 CC 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434,  
 CC 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447,  
 CC 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460,  
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 CC 1823, 1824, 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834,  
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 CC 1848, 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1857, 1858, 1859, 1860,  
 CC 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1870, 1871, 1872,  
 CC 1873, 1874, 1875, 1876, 1877, 1878, 1879, 1880, 1881, 1882, 1883, 1884,  
 CC 1885





AC R32125; (first entry)  
 DT 02-JUN-1993  
 DE Anti-IL2R alpha antibody 179 light chain variable region.  
 KW immunosuppression; tissue transplantation; graft; L chain; V region;  
 KW T-helper cell inhibition; transplant rejection; Mab;  
 KW interleukin-2 receptor.  
 FH Key Location/Qualifiers  
 FT peptide 1..20  
 FT region /label= signal  
 FT region 21..115  
 FT region /label= Variable  
 FT region 116..127  
 FT region /label= J1  
 DE4143214-A.  
 PD 28-JAN-1993.  
 PF 30-DEC-1991; 143214.  
 PR 25-JUL-1991; DE-124759.  
 PR 30-DEC-1991; DE-143214.  
 RA (BOEHR ) BOEHRINGER MANNHEIM GMBH.  
 RA Kaluza B, Riettmueller G, Scheuer W, Weidie U;  
 WPI: 93-037582/05.  
 DR N-PSDB; Q36611.  
 PT Synergistic antibody compsn. for use as immunosuppressant -  
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
 PT alpha- or anti-IL2R beta antibodies  
 PS Claim 6: Page 13; 18pp; German.  
 CC This sequence is the light chain variable region of a preferred  
 CC anti-IL2R alpha monoclonal antibody for use in the claimed  
 CC synergistic composition. Mab 179 is deposited as clone 3G10/179  
 CC (ECACC 90071905). The anti-IL2R alpha antibody is used with at least  
 CC one anti-CD4 antibody. Individually the antibodies are strongly  
 CC inhibiting and when used together their immunosuppressive properties  
 CC are improved; they synergistically inhibit T-helper cell  
 CC proliferation to effectively inhibit transplant rejection at low  
 CC doses without significantly reducing the general immune response.  
 CC See Q36607-Q36616.  
 SQ Sequence 127 AA;

## Query Match

96.3%; Score 52; DB 6; Length 127;

Best Local Similarity 88.9%; Pred. No. 3.15e+01;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 89 adyslts 97

:|||||||

QY 89 SDYSLTSS 97

arch completed: Tue Apr 20 14:09:12 1999  
 b time : 13 secs.

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MSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
on on: Tue Apr 20 13:57:31 1999; Maspar time 2.58 Seconds  
tabular output not generated. ---177.019 Million cell updates/sec

Title: >US-08-836-455-2  
Description: (50-66) from US08836455.pep (2 of 3)  
Perfect Score: 131  
Sequence: 1 GINLHWLQGEPTDKR 17

Scoring table: PAM 150  
Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot35  
1:swissprot

Statistics: Mean 28.762; Variance 43.396; scale 0.663

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	110	84.0	130	1	KV5G_MOUSE: IG KAPPA CHAIN PRECURS	1.23e-09
2	78	59.5	108	1	KV5J_MOUSE: IG KAPPA CHAIN V-V REG	4.59e-03
3	76	58.0	108	1	KV5K_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
4	76	58.0	108	1	KV5L_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
5	76	58.0	108	1	KV5M_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
6	76	58.0	108	1	KV5N_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
7	76	58.0	108	1	KV5O_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
8	70	53.4	108	1	KV5P_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
9	67	51.1	447	1	YCAL_ECOLI: HYPOTHETICAL 49.6 KD P	4.70e-01
10	67	51.1	570	1	HEMA_IAP6: HEMAGGLUTININ PRECURSO	4.70e-01
11	67	51.1	570	1	HEMA_IAPR: HEMAGGLUTININ PRECURSO	4.70e-01
12	66	50.4	346	1	UFO2_MANES: FLAVONOL 3-O-GLUCOSYL	7.02e-01
13	66	50.4	365	1	VS13_REVOL: SIGMA 3 PROTEIN (MAJOR	7.02e-01
14	66	50.4	560	1	HEMA_IAPR: HEMAGGLUTININ PRECURSO	7.02e-01
15	65	49.6	563	1	HEMA_IAPR: HEMAGGLUTININ PRECURSO	1.04e+00
16	64	48.9	108	1	KV5S_MOUSE: IG KAPPA CHAIN V-V REG	1.55e+00
17	64	48.9	108	1	KV5T_MOUSE: IG KAPPA CHAIN V-V REG	1.55e+00
18	63	48.1	108	1	KV5U_MOUSE: IG KAPPA CHAIN V-V REG	2.28e+00
19	63	48.1	108	1	KV5V_MOUSE: IG KAPPA CHAIN V-V REG	2.28e+00
20	63	48.1	255	1	YS84_CAEL: HYPOTHETICAL 29.8 KD P	2.28e+00
21	62	47.3	320	1	STBA_ECOLI: PROTEIN STBA (PARA LOC	2.28e+00
22	62	47.3	406	1	MCAL_ECOLI: PUTATIVE COLANIC ACID	3.35e+00
23	61	46.6	263	1	COO4_CAEL: UBIQUINONE BIOSYNTHESI	4.90e+00

24	61	46.6	374	1	SMF_ECOLI	SMF PROTEIN.	4.90e+00
25	61	46.6	475	1	YBES_ECOLI	HYPOTHETICAL 55.3 KD P	4.90e+00
26	61	46.6	563	1	HEMA_IAPR	HEMA_IAPR	4.90e+00
27	61	46.6	563	1	HEMA_IAPR	HEMA_IAPR	4.90e+00
28	61	46.6	780	1	YCAL_ECOLI	HYPOTHETICAL 87.3 KD P	4.90e+00
29	59	45.0	109	1	CYPC_STRA	PUTATIVE POLYPEPTIDE CY	1.03e+01
30	59	45.0	111	1	KV3E_MOUSE	IG KAPPA CHAIN V-III R	1.03e+01
31	59	45.0	119	1	Y128_SYN	HYPOTHETICAL 12.8 KD P	1.03e+01
32	59	45.0	120	1	HV3U_HUMAN	IG HEAVY CHAIN V-III R	1.03e+01
33	59	45.0	406	1	MCAL_ECOLI	PUTATIVE COLANIC ACID	1.03e+01
34	59	45.0	516	1	Y4NM_RHIS	HYPOTHETICAL 57.3 KD P	1.03e+01
35	59	45.0	570	1	HEMA_IAPR	HEMA_IAPR	1.03e+01
36	59	45.0	570	1	HEMA_IAPR	HEMA_IAPR	1.03e+01
37	59	45.0	570	1	HEMA_IAPR	HEMA_IAPR	1.03e+01
38	59	45.0	986	1	EP44_HUMAN	EPHRIIN TYPE-A RECEPTOR	1.03e+01
39	59	45.0	986	1	EP44_HUMAN	EPHRIIN TYPE-A RECEPTOR	1.03e+01
40	59	45.0	986	1	EP44_MOUSE	EPHRIIN TYPE-A RECEPTOR	1.03e+01
41	58	44.3	221	1	GSHE_RAT	EPIDIDYMAL SECRETORY G	1.49e+01
42	58	44.3	570	1	HEMA_IAPR	HEMA_IAPR	1.49e+01
43	58	44.3	570	1	HEMA_IAPR	HEMA_IAPR	1.49e+01
44	58	44.3	570	1	HEMA_IAPR	HEMA_IAPR	1.49e+01
45	58	44.3	2329	1	Y106_CAEL	HYPOTHETICAL 272.0 KD	1.49e+01

## ALIGNMENTS

Result ID	Score	Query Match	Length	ID	Description	Pred. No.
1	110	84.0	130	1	KV5G_MOUSE: IG KAPPA CHAIN PRECURS	1.23e-09
2	78	59.5	108	1	KV5J_MOUSE: IG KAPPA CHAIN V-V REG	4.59e-03
3	76	58.0	108	1	KV5K_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
4	76	58.0	108	1	KV5L_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
5	76	58.0	108	1	KV5M_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
6	76	58.0	108	1	KV5N_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
7	76	58.0	108	1	KV5O_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
8	70	53.4	108	1	KV5P_MOUSE: IG KAPPA CHAIN V-V REG	1.10e-02
9	67	51.1	447	1	YCAL_ECOLI: HYPOTHETICAL 49.6 KD P	4.70e-01
10	67	51.1	570	1	HEMA_IAP6: HEMAGGLUTININ PRECURSO	4.70e-01
11	67	51.1	570	1	HEMA_IAPR: HEMAGGLUTININ PRECURSO	4.70e-01
12	66	50.4	346	1	UFO2_MANES: FLAVONOL 3-O-GLUCOSYL	7.02e-01
13	66	50.4	365	1	VS13_REVOL: SIGMA 3 PROTEIN (MAJOR	7.02e-01
14	66	50.4	560	1	HEMA_IAPR: HEMAGGLUTININ PRECURSO	7.02e-01
15	65	49.6	563	1	HEMA_IAPR: HEMAGGLUTININ PRECURSO	1.04e+00
16	64	48.9	108	1	KV5S_MOUSE: IG KAPPA CHAIN V-V REG	1.55e+00
17	64	48.9	108	1	KV5T_MOUSE: IG KAPPA CHAIN V-V REG	1.55e+00
18	63	48.1	108	1	KV5U_MOUSE: IG KAPPA CHAIN V-V REG	2.28e+00
19	63	48.1	108	1	KV5V_MOUSE: IG KAPPA CHAIN V-V REG	2.28e+00
20	63	48.1	255	1	YS84_CAEL: HYPOTHETICAL 29.8 KD P	2.28e+00
21	62	47.3	320	1	STBA_ECOLI: PROTEIN STBA (PARA LOC	2.28e+00
22	62	47.3	406	1	MCAL_ECOLI: PUTATIVE COLANIC ACID	3.35e+00
23	61	46.6	263	1	COO4_CAEL: UBIQUINONE BIOSYNTHESI	4.90e+00

Query Match

Best Local Similarity 84.0%; Score 110; DB 1; Length 130;

Pred. No. 1.23e-09;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 52 GSSLNMLQOEPRDGTIK 68  
 1:|||||  
 QY 50 GINLHMLQOEPRDGTIK 66

RESULT 2  
 ID KVSJ\_MOUSE STANDARD; PRT; 108 AA.

AC P01643;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-V REGION (MOPC 173).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; RODENTIA.

SEQUENCE.  
 MEDLINE: 76091934.

RL EUR. J. BIOCHEM. 59:525-537(1975).  
 - THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR: A01926; KMS73.  
 KW IMMUNOGLOBULIN V REGION.

FT DOMAIN 1 23  
 FT DOMAIN 2 34  
 FT DOMAIN 3 49  
 FT DOMAIN 4 56  
 FT DOMAIN 5 57  
 FT DOMAIN 6 88  
 FT DOMAIN 7 97  
 FT DOMAIN 8 98  
 FT DOMAIN 9 108  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11819 MW; EA186054 CRC32;

Query Match  
 Best Local Similarity 59.5%; Score 78; DB 1; Length 108;  
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 30 GNYLWYQQRPGTVK 45  
 1:|||||  
 QY 50 GINLHMLQOEPRDGTIK 65

RESULT 3  
 ID KVSJ\_MOUSE STANDARD; PRT; 108 AA.

AC P01646;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-V REGION (HP 123E6).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; RODENTIA.

SEQUENCE.  
 MEDLINE: 82150934.  
 RA SIEGELMAN M., CAPRA J.D.;  
 PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).  
 - ANTI-ARSONATE HYBRIDOMA PROTEIN.  
 DR PIR: A01927; KMSAR.  
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.

FT DOMAIN 1 23  
 FT DOMAIN 2 34  
 FT DOMAIN 3 49  
 FT DOMAIN 4 56  
 FT DOMAIN 5 57  
 FT DOMAIN 6 88  
 FT DOMAIN 7 97  
 FT DOMAIN 8 98  
 FT DOMAIN 9 108  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11819 MW; EA186054 CRC32;

FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11989 MW; 23B8B67 CRC32;

Query Match  
 Best Local Similarity 58.0%; Score 76; DB 1; Length 108;  
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 33 LNWYQQRPGTVK 45  
 1:|||||  
 QY 53 LHWLQOEPRDGTIK 65

RESULT 4  
 ID KVSJ\_MOUSE STANDARD; PRT; 108 AA.

AC P04946;  
 DT 13-AUG-1987 (REL. 05, CREATED)  
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-V REGION (MOS-89.4).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; RODENTIA.

SEQUENCE FROM N.A.  
 RX MEDLINE: 83271467.  
 RA KARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;  
 NATURE 304:320-324(1983).  
 - ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.  
 DR EMBL: K00745; G196455; -  
 DR HSSP: P01607; 1FAI.  
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.

FT DOMAIN 1 23  
 FT DOMAIN 2 34  
 FT DOMAIN 3 49  
 FT DOMAIN 4 56  
 FT DOMAIN 5 57  
 FT DOMAIN 6 88  
 FT DOMAIN 7 97  
 FT DOMAIN 8 98  
 FT DOMAIN 9 107  
 FT DISULFID 107  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11866 MW; D396F142 CRC32;

Query Match  
 Best Local Similarity 58.0%; Score 76; DB 1; Length 108;  
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 33 LNWYQQRPGTVK 45  
 1:|||||  
 QY 53 LHWLQOEPRDGTIK 65

RESULT 5  
 ID KVSJ\_MOUSE STANDARD; PRT; 108 AA.

AC P01645;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-V REGION (HP 93677).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; RODENTIA.

SEQUENCE.  
 MEDLINE: 82150934.  
 RA SIEGELMAN M., CAPRA J.D.;  
 PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).  
 - ANTI-ARSONATE HYBRIDOMA PROTEIN.  
 DR PIR: A01927; KMSAR.  
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.

FT DOMAIN 1 23  
 FT DOMAIN 2 34  
 FT DOMAIN 3 49  
 FT DOMAIN 4 56  
 FT DOMAIN 5 57  
 FT DOMAIN 6 88  
 FT DOMAIN 7 97  
 FT DOMAIN 8 98  
 FT DOMAIN 9 108  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11819 MW; EA186054 CRC32;

```

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11954 MW: A203EL30 CRC32:

Query Match
Best Local Similarity 69.2%; Score 76; DB 1; Length 108;
Pred. No. 1.10e-02;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 33 LHWYQKPDGTVK 45
1:1111111111
53 LHWLOQEPDGTIK 65

RESULT 6
AC KVS_MOUSE STANDARD: PRT: 108 AA.
P01644:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (HP R16.7).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX STRAIN-A/J;
RX MEDLINE: 82150934.
RA SIEGELMAN M., CAPRA J.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC -1- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVSAR.
DR HSSP: P01607; 1FAI.
KW IMMUNOGLOBULIN V REGION; ANTIRSONATE ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11910 MW: 64A62905 CRC32:

Query Match
Best Local Similarity 58.0%; Score 76; DB 1; Length 108;
Pred. No. 1.10e-02;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 33 LHWYQKPDGTVK 45
1:1111111111
53 LHWLOQEPDGTIK 65

RESULT 7
AC KVS_MOUSE STANDARD: PRT: 108 AA.
P01647:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (HP 124E1).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX STRAIN-A/J;
RX MEDLINE: 82150934.

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RA SIEGELMAN M., CAPRA J.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC -1- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVSAR.
DR HSSP: P01607; 1FAI.
KW IMMUNOGLOBULIN V REGION; ANTIRSONATE ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11965 MW: 84754175 CRC32:

Query Match
Best Local Similarity 58.0%; Score 76; DB 1; Length 108;
Pred. No. 1.10e-02;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 33 LHWYQKPDGTVK 45
1:1111111111
53 LHWLOQEPDGTIK 65

RESULT 8
AC KVS_MOUSE STANDARD: PRT: 108 AA.
P01648:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (HP 91A3).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX STRAIN-A/J;
RX MEDLINE: 82150934.
RA SIEGELMAN M., CAPRA J.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC -1- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVSAR.
DR HSSP: P01607; 1FAI.
KW IMMUNOGLOBULIN V REGION; ANTIRSONATE ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11961 MW: 58067780 CRC32:

Query Match
Best Local Similarity 53.4%; Score 70; DB 1; Length 108;
Pred. No. 1.38e-01;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 33 LHWYQKPDGTVK 45
1:1111111111
53 LHWLOQEPDGTIK 65

RESULT 9
AC YCAI_ECOLI STANDARD: PRT: 447 AA.
P45526: P75833;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 49.6 KD PROTEIN IN LOLA-SENS INTERGENIC REGION.

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GN YCAJ.  
 OS ESCHERICHIA COLI.  
 OC PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC ENTEROBACTERIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RA BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;  
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [2]  
 RP SEQUENCE OF 1-61 FROM N.A.  
 RC STRAIN-K12 / MC4100;  
 RA MATSUYAMA S.-I., TAJIMA T., TOKUDA H.;  
 RL EMO J. 14:3365-3372(1995).  
 RN [3]  
 RP SEQUENCE OF 367-447 FROM N.A.  
 RC STRAIN-K12;  
 RA MEDLINE: 87146412.  
 HAERTLEIN M., MADERN D., LEBERMAN R.;  
 NUCLEIC ACIDS RES. 15:1005-1017(1987).  
 RN [4]  
 RP IDENTIFICATION.  
 RA MEDLINE: 96032851.  
 BORODOVSKY M., MCININCH J., KOONIN E.V., RUDD K.E., MEDIGUE C.,  
 DANCHIN A.;  
 NUCLEIC ACIDS RES. 23:3554-3562(1995).  
 CC -1- SIMILARITY: STRONG, TO H. INFLUENZA H1590 AND C. BURNETTII HOMOLOG.  
 CC -1- SIMILARITY: TO YEAST INL218W.  
 CC -1- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  
 FRAMESHIFT IN POSITION 370.  
 DR EMBL: AE000191; G1787119; -;  
 DR EMBL: D49398; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: X05017; -; NOT\_ANNOTATED\_CDS.  
 DR ECGENE: EG12690; YCAJ.  
 KW HYPOTHEICAL PROTEIN; ATP-BINDING.  
 FT NP-BIND 57  
 SQ SEQUENCE 447 AA; 49626 MW; 0865785D CRC32;  
 FT  
 Query Match 51.1%; Score 67; DB 1; Length 447;  
 Best Local Similarity 44.4%; Pred. No. 4.70e-01;  
 Matches 8; Conservative 5; Mismatches 4; Indels 1; Gaps 1;  
 Db 428 GEXLWLAEDONSPIK 445  
 QY 50 GINLHML-QOEPOGTIKR 66  
 ID HEMA\_IHNC6 STANDARD; PRT; 570 AA.  
 AC P26094;  
 DT 01-MAY-1992 (REL. 22, CREATED)  
 DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE HEMAGGLUTININ PRECURSOR.  
 GN HA.  
 OS INFLUENZA A VIRUS (STRAIN A/EQUINE/CAMBRIDGE/1/63).  
 OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 92230399.  
 GIBSON C.A., DANIELS R.S., OXFORD J.S., MCCAULEY J.W.;  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
 CELL RECEPTORS AND FOR INITIATING INFECTION.  
 CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAINS  
 (HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
 DR EMBL: X62553; G59190; -;  
 DR PIR: S22013; S22013.  
 DR HSSP: P03437; 1HGD.  
 KW ENVELOPE PROTEIN; HEMAGGLUTININ; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1  
 FT CHAIN 19 345 HA1 CHAIN.

FT CHAIN 350 570 HA2 CHAIN.  
 FT CARBOHYD 30 30 POTENTIAL.  
 FT CARBOHYD 46 46 POTENTIAL.  
 FT CARBOHYD 249 249 POTENTIAL.  
 FT CARBOHYD 431 431 POTENTIAL.  
 FT CARBOHYD 503 503 POTENTIAL.  
 SQ SEQUENCE 570 AA; 64151 MW; E4E3F882 CRC32;  
 FT  
 Query Match 51.1%; Score 67; DB 1; Length 570;  
 Best Local Similarity 42.9%; Pred. No. 4.70e-01;  
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 Db 239 IDPHWMLDNDPTV 252  
 QY 51 INLHMLQOEPOGTI 64  
 ID HEMA\_IHNC6 STANDARD; PRT; 570 AA.  
 AC P26101;  
 DT 01-MAY-1992 (REL. 22, CREATED)  
 DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE HEMAGGLUTININ PRECURSOR.  
 GN HA.  
 OS INFLUENZA A VIRUS (STRAIN A/EQUINE/PRAGUE/1/56).  
 OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 92230399.  
 GIBSON C.A., DANIELS R.S., OXFORD J.S., MCCAULEY J.W.;  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
 CELL RECEPTORS AND FOR INITIATING INFECTION.  
 CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAINS  
 (HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
 DR EMBL: X62552; G59204; -;  
 DR PIR: A45591; A45591.  
 DR HSSP: P03437; 1HGD.  
 KW ENVELOPE PROTEIN; HEMAGGLUTININ; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1  
 FT CHAIN 19 345 HA1 CHAIN.  
 FT CHAIN 350 570 HA2 CHAIN.  
 FT CARBOHYD 30 30 POTENTIAL.  
 FT CARBOHYD 46 46 POTENTIAL.  
 FT CARBOHYD 167 167 POTENTIAL.  
 FT CARBOHYD 249 249 POTENTIAL.  
 FT CARBOHYD 431 431 POTENTIAL.  
 FT CARBOHYD 503 503 POTENTIAL.  
 SQ SEQUENCE 570 AA; 64139 MW; 399E8F59 CRC32;  
 FT  
 Query Match 51.1%; Score 67; DB 1; Length 570;  
 Best Local Similarity 42.9%; Pred. No. 4.70e-01;  
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 Db 239 IDPHWMLDNDPTV 252  
 QY 51 INLHMLQOEPOGTI 64  
 ID UPO2\_MANES STANDARD; PRT; 346 AA.  
 AC 040285;  
 DT 01-NOV-1997 (REL. 35, CREATED)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 2 (EC 2.4.1.91) (UDP-GLUCOSE  
 GT2 OR UGT73A2.  
 OS MANIHOT ESCULENTA (CASSAVA) (MANIOC).  
 OC EUPHAROTIA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;  
 GN EUPHORBIALES; EUPHORBIAEAE.  
 RN [1]

RC	SEQUENCE FROM N.A.
RH	TISSUE-COTYLEDON.
RA	MEDLINE; 95201291.
RL	HUGHES J., HUGHES M.A.;
RM	DNA SEQ. 5:41-49(1994).
RR	-1 FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, THIS
RS	GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANIN
RT	PIGMENTS (BY SIMILARITY).
RU	-1 CATALYTIC ACTIVITY: UDP-GLUCOSE + A FLAVONOL -> UDP + FLAVONOL
RV	3-O-D-GLUCOSIDE.
RW	-1 PATHWAY: ONE OF THE ESSENTIAL AND TERMINAL STEPS IN THE
RX	ANTHOXANIN BIOSYNTHETIC PATHWAY.
RY	-1 TISSUE SPECIFICITY: EXPRESSED IN COTYLEDONS, ROOTS AND LEAVES.
RZ	-1 DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION IN COTYLEDONS THAT JUST
SA	EMERGED FROM THE SEED COAT. LOW LEVELS IN HYPOCOTYLS AND
SB	INCREASING LEVELS IN ROOTS THROUGHOUT THIS PERIOD OF DEVELOPMENT.
SC	-1 SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
SD	EMBL; X77461. G453255. -
SE	PROSITE; PS00375. UDRGT.1
SF	TRANSFERASE; GLYCOSYLTRANSFERASE; MULTIGENE FAMILY.
SG	NON_TER
SH	SEQUENCE 346 AA; 38834 MW; 6E8242F0 CRC32;
SI	1
SJ	1
SK	Query Match
SL	Best Local Similarity 33.3%; Score 66; DB 1; Length 346;
SM	Matches 4; Conservative 8; Mismatches 0; Indels 0; Gaps 0
SN	Db 136 MOWLDQPEGSV 147
SO	53 LHWLQDPPDGTI 64
SP	Result 13
SR	ID VS13_REV01 STANDARD; PRT; 365 AA.
SS	AC P07939;
ST	DT 01-AUG-1988 (REL. 08, CREATED)
SU	DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
SV	DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
SW	DE SIGMA 3 PROTEIN (MAJOR OUTER CAPSID PROTEIN).
SX	GN S4.
SY	OS REVORUS (TYPE 1 / STRAIN LANG).
SZ	NC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; PROVIRIDAE; REVIRUSS.
TB	CC [1]
TC	RP SEQUENCE FROM N.A.
TD	RA MEDLINE; 86215171.
TE	RA ATWATER J.A., MANEWITSU S.M., SAMUEL C.E.;
TF	RL BIOCHEM. BIOPHYS. RES. COMMUN. 136:183-192(1986).
TG	[2]
TH	SEQUENCE FROM N.A.
TI	KX MEDLINE; 92142506.
TJ	RA SELINGER I.S., GIANNINI M., SHATKIN A.J.;
TK	RL VIRIOLOGY 187:202-210(1992).
TL	-1 FUNCTION: THE VIRAL OUTER SHELL POLYPEPTIDES, OF WHICH SIGMA-3 IS
TM	ONE, IMPOSE STRUCTURAL CONSTRAINTS THAT PREVENT ELONGATION OF
TN	SIGMA-3 TRANSCRIPTS BY THE VIRION-ASSOCIATED RNA-POLYMERASE.
TO	CC SIGMA-3 ALSO INHIBITS HOST PROTEIN SYNTHESIS IN INFECTED MOUSE L
TP	CELLS AND MAY BE INVOLVED IN SWITCHING FROM CELLULAR TO VIRAL MRNA
TQ	TRANSLATION AT LATE TIMES AFTER INFECTION.
TR	CC EMBL; M13139. G333720. -
TS	DR EMBL; X61586; G61946; -
TT	DR PIR; A24245; MNKR54.
TU	DR PIR; A42192; A42192.
TV	KW COAT PROTEIN.
TV	FT CONFLICT
TX	SEQ SEQUENCE 325 D -> N (IN REF. 2).
TY	365 AA; 41156 MW; B001989A CRC32;
TA	Query Match
TB	Best Local Similarity 33.3%; Score 66; DB 1; Length 365;
TC	Matches 5; Conservative 8; Mismatches 2; Indels 0; Gaps 0
TD	Db 129 VELMWLOYDPNSMR 143
TE	51 INLHWLQDPPDGTI 65
TF	Result 13
TF	ID VS13_REV01 STANDARD; PRT; 365 AA.
TF	AC P07939;
TF	DT 01-AUG-1988 (REL. 08, CREATED)
TF	DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
TF	DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
TF	DE SIGMA 3 PROTEIN (MAJOR OUTER CAPSID PROTEIN).
TF	GN S4.
TF	OS REVORUS (TYPE 1 / STRAIN LANG).
TF	NC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; PROVIRIDAE; REVIRUSS.
TF	CC [1]
TF	RP SEQUENCE FROM N.A.
TF	RA MEDLINE; 86215171.
TF	RA ATWATER J.A., MANEWITSU S.M., SAMUEL C.E.;
TF	RL BIOCHEM. BIOPHYS. RES. COMMUN. 136:183-192(1986).
TF	[2]
TF	SEQUENCE FROM N.A.
TF	KX MEDLINE; 92142506.
TF	RA SELINGER I.S., GIANNINI M., SHATKIN A.J.;
TF	RL VIRIOLOGY 187:202-210(1992).
TF	-1 FUNCTION: THE VIRAL OUTER SHELL POLYPEPTIDES, OF WHICH SIGMA-3 IS
TF	ONE, IMPOSE STRUCTURAL CONSTRAINTS THAT PREVENT ELONGATION OF
TF	SIGMA-3 TRANSCRIPTS BY THE VIRION-ASSOCIATED RNA-POLYMERASE.
TF	CC SIGMA-3 ALSO INHIBITS HOST PROTEIN SYNTHESIS IN INFECTED MOUSE L
TF	CELLS AND MAY BE INVOLVED IN SWITCHING FROM CELLULAR TO VIRAL MRNA
TF	TRANSLATION AT LATE TIMES AFTER INFECTION.
TF	CC EMBL; M13139. G333720. -
TF	DR EMBL; X61586; G61946; -
TF	DR PIR; A24245; MNKR54.
TF	DR PIR; A42192; A42192.
TF	KW COAT PROTEIN.
TF	FT CONFLICT
TF	SEQ SEQUENCE 325 D -> N (IN REF. 2).
TF	365 AA; 41156 MW; B001989A CRC32;
TF	Query Match
TF	Best Local Similarity 33.3%; Score 66; DB 1; Length 365;
TF	Matches 5; Conservative 8; Mismatches 2; Indels 0; Gaps 0
TF	Db 129 VELMWLOYDPNSMR 143
TF	51 INLHWLQDPPDGTI 65
TF	Result 13
TF	ID VS13_REV01 STANDARD; PRT; 365 AA.
TF	AC P07939;
TF	DT 01-AUG-1988 (REL. 08, CREATED)
TF	DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
TF	DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
TF	DE SIGMA 3 PROTEIN (MAJOR OUTER CAPSID PROTEIN).
TF	GN S4.
TF	OS REVORUS (TYPE 1 / STRAIN LANG).
TF	NC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; PROVIRIDAE; REVIRUSS.
TF	CC [1]
TF	RP SEQUENCE FROM N.A.
TF	RA MEDLINE; 86215171.
TF	RA ATWATER J.A., MANEWITSU S.M., SAMUEL C.E.;
TF	RL BIOCHEM. BIOPHYS. RES. COMMUN. 136:183-192(1986).
TF	[2]
TF	SEQUENCE FROM N.A.
TF	KX MEDLINE; 92142506.
TF	RA SELINGER I.S., GIANNINI M., SHATKIN A.J.;
TF	RL VIRIOLOGY 187:202-210(1992).
TF	-1 FUNCTION: THE VIRAL OUTER SHELL POLYPEPTIDES, OF WHICH SIGMA-3 IS
TF	ONE, IMPOSE STRUCTURAL CONSTRAINTS THAT PREVENT ELONGATION OF
TF	SIGMA-3 TRANSCRIPTS BY THE VIRION-ASSOCIATED RNA-POLYMERASE.
TF	CC SIGMA-3 ALSO INHIBITS HOST PROTEIN SYNTHESIS IN INFECTED MOUSE L
TF	CELLS AND MAY BE INVOLVED IN SWITCHING FROM CELLULAR TO VIRAL MR

RESULT	14	STANDARD;	PRT;	560 AA.
ID	HEMA IATKR			
AC	P03458;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)			
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)			
DE	HEMAGGLUTININ PRECURSOR.			
GN	HA.			
OS	INFLUENZA A VIRUS (STRAIN A/TURKEY/OREGON/71).			
OC	VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 90266469.			
RA	ORLICH M., KHATCHIRIAN D., TEIGLER A., ROTT R.;			
RL	VIROLOGY 176:531-538(1990).			
RN	[2]			
RP	SEQUENCE OF 1-108 FROM N.A.			
RX	MEDLINE; 82150925.			
RA	AIR G.M.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7639-7643(1981).			
CC	-1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.			
CC	-1- SUBUNIT: HOMOTETMER, EACH OF THE MONOMER IS FORMED BY TWO CHAINS			
CC	(HA1 AND HA2) LINKED BY A DISULFIDE BOND.			
CC	EMBL; M31889; G323975; -.			
DR	EMBL; J02164; G324163; -.			
DR	PIR; A34772; HMV177.			
DR	PIR; A04069; A04069.			
DR	HSSP: P03437; 1HGd.			
KW	ENVELOPE PROTEIN; HEMAGGLUTININ; GLYCOPROTEIN; SIGNAL.			
FT	SIGNAL	1	18	
FT	CHAIN	19	338	HA1 CHAIN.
FT	CHAIN	340	560	HA2 CHAIN.
FT	CARBOHYD	30	30	POTENTIAL.
FT	CARBOHYD	46	46	POTENTIAL.
FT	CARBOHYD	249	249	POTENTIAL.
FT	CARBOHYD	421	421	POTENTIAL.
FT	CARBOHYD	493	493	POTENTIAL.
FT	CONFLICT	60	60	S -> C (IN REF. 2).
FT	CONFLICT	92	92	S -> L (IN REF. 2).
FT	CONFLICT	103	103	D -> N (IN REF. 2).
FT	CONFLICT	103	103	D -> N (IN REF. 2).
SO	SEQUENCE	560 AA;	62013 MM;	74DE95A9 CRC32;
Query Match		50.4%;	Score 66;	DB 1; Length 560;
Best Local Similarity		42.9%;	Pred. No. 7.02e-01;	
Matches	6;	Conservative	5;	Mismatches 3; Indels 0; Gaps 0;
Db	239 IDHFWLLDPNDTV	252		
Oy	1::111::1::1:			
	51 INLHWLQOEFDGTI	64		
RESULT	15	STANDARD;	PRT;	563 AA.
ID	HEMA IAFPR			
AC	P03459;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)			
DE	HEMAGGLUTININ PRECURSOR.			
GN	HA.			
OS	INFLUENZA A VIRUS (STRAIN A/FOWL PLAGUE VIRUS/ROSTOCK/34).			
OC	VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 80054765.			
RA	PORTER A.G., BARBER C., CAREY N.H., HALLEWELL R.A., THRELFALL G.,			
RA	EMAGE J.S.;			
RL	NATURE 282:471-477(1979).			
RN	[2]			
RP	MUTANTS T51 AND TS227.			
RX	MEDLINE; 87080266.			

RA SCHUY W., WILL C., KURODA K., SCHOLTESSEK C., GARTEN W., KLENK H.-D.;  
 RL EMBO J. 5:2831-2836(1986).  
 RN [3]  
 RP STRUCTURE OF CARBOHYDRATES ON ASN-424 AND ASN-496.  
 RA GEYER R., DIABATE S., GEYER H., KLENK H.-D., NIEMANN H., STIRM S.;  
 RL GLYCOCOMJ. J. 4:17-32(1987).  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
 CELL RECEPTORS AND FOR INITIATING INFECTION.  
 CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAINS  
 (HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
 CC -1- PTM: CLEAVAGE OF HEMAGGLUTININ INTO TWO SUBUNITS, HA1 AND HA2,  
 USUALLY TAKES PLACE EITHER ON SMOOTH INTERNAL MEMBRANES OR AT  
 THE PLASMA MEMBRANE; THIS STEP IS ESSENTIAL FOR INFECTIVITY AND  
 PROBABLY ALSO FOR PATHOGENICITY.  
 CC -1- MUTANTS TS1 AND TS227 HAVE A TEMPERATURE SENSITIVE DEFECT IN  
 THE TRANSPORT OF THE HEMAGGLUTININ FROM THE ROUGH ENDOPLASMIC  
 RETICULUM TO THE GOLGI APPARATUS.  
 CC EMBL, V01105; G60807; -.  
 CC PIR; A04070; HMIVF.  
 CC HSSP; P03437; 1HGD.  
 DR ENVELOPE PROTEIN; HEMAGGLUTININ; GLYCOPROTEIN; SIGNAL.

FT SIGNAL	1	18	
FT CHAIN	19	336	HA1 CHAIN.
FT PROPEP	337	342	CONNECTING PEPTIDE.
FT CHAIN	343	563	HA2 CHAIN.
FT CARBOHYD	30	30	
FT CARBOHYD	46	46	
FT CARBOHYD	141	141	
FT CARBOHYD	167	167	
FT CARBOHYD	249	249	
FT CARBOHYD	424	424	
FT CARBOHYD	475	475	OLIGOMANNOSIDIC.
FT CARBOHYD	496	496	IN MUTANT TS227.
FT VARIANT	113	113	OLIGOMANNOSIDIC.
FT VARIANT	293	293	E -> G (IN MUTANT TS227).
FT VARIANT	416	416	S -> G (IN MUTANT TS1).
FT VARIANT	475	475	E -> G (IN MUTANT TS1).
FT VARIANT	475	475	D -> N (IN MUTANT TS227).
SO SEQUENCE	563 AA;	62702 MW;	E543081E CRC32;

Query Match 49.6%; Score 65; DB 1; Length 563;  
 Best Local Similarity 42.9%; Pred. No. 1.04e+00;  
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 239 IDFWLILDPNDTV 252  
 QY 51 INLHWLQOEPDGTI 64

Job completed: Tue Apr 20 13:57:38 1999  
 Job time : 7 secs.